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Sort By:
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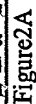
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Figure 1



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316 page(s) | 6310 row(s)

Links	Source DB	Code	Description	Organism	Length	Query Region	Target Region	Cluster	% Align ID	Align Score	Align Length	Confidence
PSO P5A XR DP	GenBank	AA066138.1	Hypothetical protein T7787...	Ceenorhabditis elegans	424	29-240	185-419	AA066138.1	11.60	256	252	100
PSO P5A XR DP	GenBank	AA053273.1	mineralocorticoid receptor	Sinuostoma	164	75-232	1-159	AA053273.1	19	256	163	100
PSO P5A XR DP	GenBank	CAA05410.2	receptor	Homo sapiens	614	15-247	394-604	CAA05410.2	14.60	256	239	100
PSO P5A XR DP	GenBank	CAB00123.1	Not given	Ceenorhabditis elegans	406	17-240	184-405	CAB00123.1	16.60	255	229	100
PSO P5A XR DP	GenBank	AAA81156.1	Hypothetical protein CS021...	Ceenorhabditis elegans	547	6-240	283-444	AAA81156.1	14.40	255	257	100
PSO P5A XR DP	GenBank	CAC42097.1	ERbeta protein	Canis familiaris	250	1-107	142-247	CAC42097.1	60.70	255	107	100
PSO P5A XR DP	GenBank	AA015179.1	nuclear receptor NHR-88	Ceenorhabditis elegans	598	7-238	101-423	AA015179.1	15.40	254	240	100
PSO P5A XR DP	GenBank	AA015180.1	nuclear receptor NHR-90	Ceenorhabditis elegans	408	30-239	177-400	AA015180.1	12.10	254	231	100
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PSO P5A XR DP	GenBank	CAC02968.1	peroxisome proliferator ac...	Salmo salar	482	4-204	229-480	CAC02968.1	16.40	253	214	100
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PSO P5A XR DP	GenBank	AA052312.1	Hypothetical protein C03G6...	Ceenorhabditis elegans	430	1-241	105-400	AA052312.1	15.40	251	259	100
PSO P5A XR DP	GenBank	CAA16293.1	Not given	Ceenorhabditis elegans	270	2-239	9-267	CAA16293.1	12	250	266	100

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Figure 2B

Figure 2C



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NCBI CD-Search Entrez

REF-FAST 2.2.2 [Dec-14-2001]
Query: local sequence: g14753768[emb] [GAM5410.2] protein [Homo sapiens] (514 letters)
Database: cspis esp vl 54
3693 PSSMs: 718, 011 total columns

Mouse-over boxes to display more information

NEW SHOW other proteins containing these domains

.. This CD alignment includes 3D structure. To display structure, download [Cn3D v3.0.0!](#)

PSSMs producing significant alignments:

	Score E (bits) value
g14753768[emb] Znf_C4, c4 zinc finger in nuclear hormone receptors	51.2 2e-10
g14753768[emb] Zf-C4, Zinc finger, C4 type (two domains). In nearly all cases...	56.6 4e-09
g14753768[emb] Znf_C4, c4 zinc finger in nuclear hormone receptors	

Add query to multiple alignment, display up to 10 sequences most similar to the query

CD-length = 73 residues, 94.5% aligned
Score = 61.2 bits (147), Expect = 2e-10

Query: 304 LGVYVYASSTVVSCEATYFPRSS-OFSTPAC-FRQDNIISNRKSCAP-LL 360
Subject: 4 PMLVQDASSTVVSCEATYFPRSS-OFSTPAC-FRQDNIISNRKSCAP-LL 63

Query: 351 RLKPSINE 369
Subject: 64 KLEFVDRP 72

g14753768[emb] Zf-C4, Zinc finger, C4 type (two domains). In nearly all cases, this is the DNA binding domain of a nuclear hormone receptor. The alignment contains two Zinc finger domains that are too dissimilar to be aligned with each other.

Add query to multiple alignment, display up to 10 sequences most similar to the query

CD-length = 76 residues, 82.9% aligned
Score = 56.6 bits (135), Expect = 4e-09

Query: 304 LGVYVYASSTVVSCEATYFPRSS-OFSTPAC-FRQDNIISNRKSCAP-LL 360
Subject: 64 KLEFVDRP 72

Document: Doria 0.453 sec

Figure 4

[illegible]

Figure 5A

Entry Page - Netscape 6
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http://rs.ebi.ac.uk/rsbin/cgi-bin/wget2-14-3/CoW/1a/WP-Hsval-Acchumber0432451-9
 Home Netscape Search Shop Bookmarks Tools Families ChIPinformatics ChNCBI Mouse Lys ChTransc ChProtein ChGenome Centres

(1996) *Cancer Data* 1996: 20:94-102

Position: SEQUENCE FROM N.A.
 Comments: TISSUE-BREAST;
 Medline: 96253999
 PubMed: 8706045

[2] Hamaek, M.E., Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 Position: SEQUENCE FROM N.A.
 Comments: TISSUE-BREAST;

Comments: NUCLEAR (BY SIMILARITY).
 LOCATION: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.

SIMILARITY

Databases cross-references

EMBL: AJ002425; CAA05410.2; --
 HSSP: P03372; IHCO.
 InterPro: IPR001628; ZnF_C4sterad.
 Pfam: PF00105; zf-C4_1.
 ProDom: PD000095; zf-C4_1.
 SMART: SM00399; ZnF_C4_1.

Keywords: DNA-binding; Nuclear receptor; Transcription regulation; Zinc-finger.

Sequence information

Length: 614 aa, molecular weight: 68619 Da, CRC64 checksum: F7B57067C7FFB18

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 KRAKAGTQ LQALVAKAL TFAFSSTPR QSLKATVD ELYKVESGP 180
 WTCEDQRO VNPDPYVQ DILQDGLP QYVAVRQ EKAATPW KQKQVRRG 240
 AQSGLZLY TQKQDQHS SAKVQVET EASSTQVAC FVNDQVSR KNSDPAQL 300
 KQVQVQVQ YKQVQVQV SAKVQVET EASSTQVAC FVNDQVSR KNSDPAQL 360
 RLQVSTIKI KNSDPAQL RNSDPAQL RNSDPAQL RNSDPAQL RNSDPAQL 420
 QKQVQVSR RNSDPAQL RNSDPAQL RNSDPAQL RNSDPAQL RNSDPAQL 480
 STPLFVQSH KNSDPAQL RNSDPAQL RNSDPAQL RNSDPAQL RNSDPAQL 540
 TEDIQDQHS QYVAVRQV EKAATPW KQKQVRRG KNSDPAQL KNSDPAQL 600
 TQKQDQHS SAKVQVET EASSTQVAC FVNDQVSR KNSDPAQL KNSDPAQL 614
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General Description References Comments Links Keyword Sequence

SRS 6.1.3 | feedback

Document Date: 27/10/2004

Figure 5B

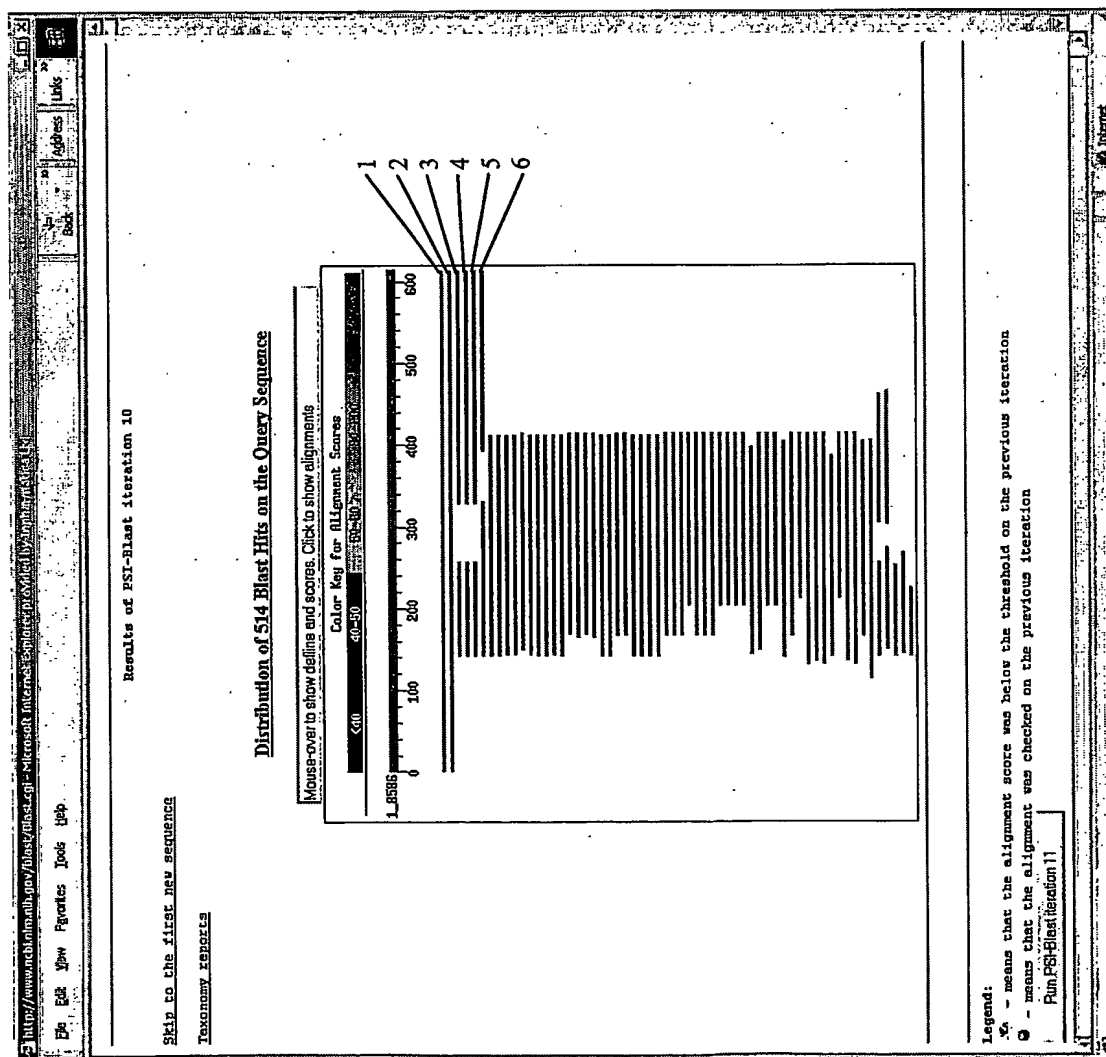


Figure 5C

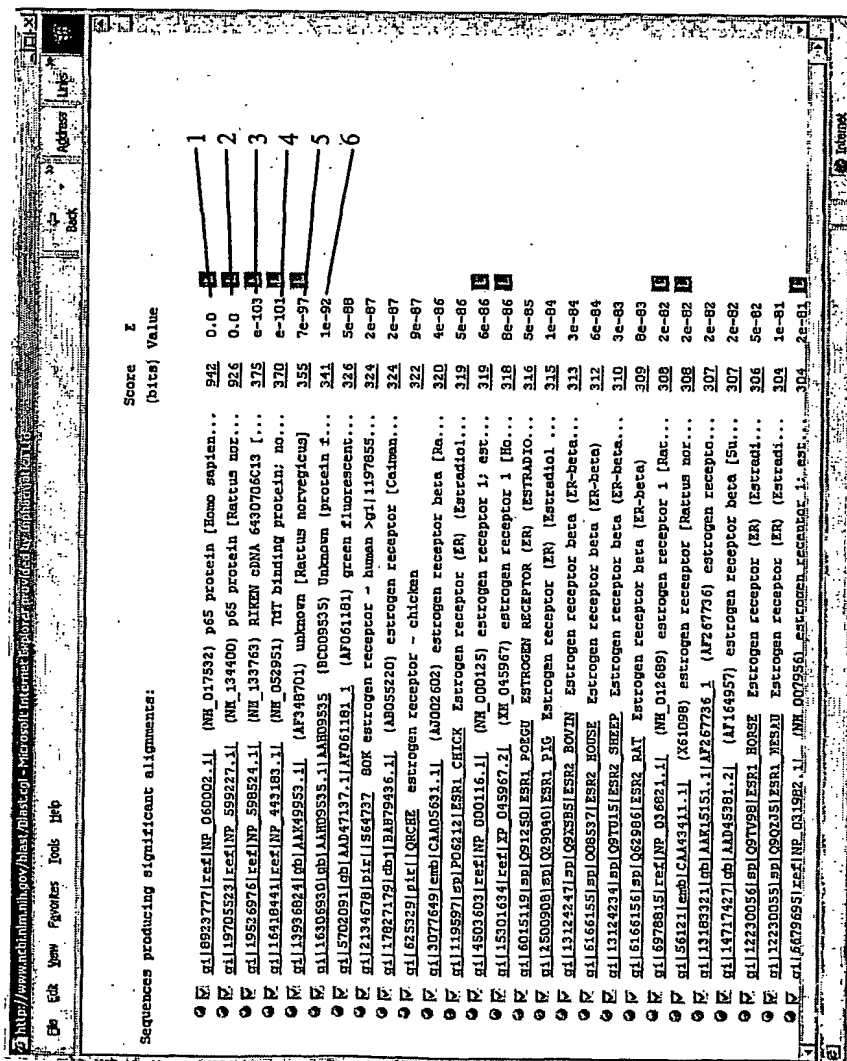
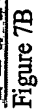


Figure 5D

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Home Netscape Search Stop Bookmarks Tools Families Elpharmatica ENCB Mouse Links Transc ERF Protein Genome Centres

Relationship Results
Accession Code: CAA054102
Search:
Search in: Source DB column for
PAGES: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 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2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635

Figure 7A



CAA05410.2 3ERT	MGPENESVGGEMWGRVCFVSARQKPRCSTINSLVARTCYNMIALVDWIEQDFKSTWR 60 -----
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CAA05410.2 3ERT	VNICEGKRGVGIHPPDNYGDTLDENLGLPQKIVIKVPQTEEANTWLRQDLKNHNSAKE 240 -----
CAA05410.2 3ERT	AGGSDEIKTFVTGCKKGDSGRKNMTTHDRNSKKWRVNLISMASLQLDSRGRAGPRRG 300 -----
CAA05410.2 3ERT	ARRLCLVCEDYASCSNCTVWSCAYKVFRRSQSFTDPACFTDNCISKNRSKSCPACLL 360 -----
CAA05410.2 3ERT	RCLHPSINEIRKDKRAALKVRDNVGVEVDMTGPSWTCLKLLFSDGEKVIPLRGHELPGIK 420 -----LALSLTADQMVSAALLDAEPPILYSEYDPTFPFSEASMMGLL 346
CAA05410.2 3ERT	GGRQAKQQSHRGSPIPKNRKGWPPGHHVLSNDGGAGGRVWKKKCKPIRREGPKWWDRLN- 479 TNLADREL VH-MINWAKRVPGFVDLTLDQVHLLCEAWLEILMIGLVWRSMEHPGKLLFA 405
CAA05410.2 3ERT	-----ESTPLFWGSRANKSLGKGTRGRIFIKHPLHFKFAADPQDK-- 520 PNLLLDNRNQKCVEGMVEIFDMLLATSS--RFRMNLQGEFVCLKSIILLNSGVYTFLS 463
CAA05410.2 3ERT	---HWLAEQHHMRATGGK---MAYLLIEEDIG- QHHGQ GFPV MLIKI SHIRHMVGGVAH 572 STLKSLEEKDHIHRVLDKITDTLILHMAKAGLT QOQH RLAQL LLIL SHIRHMSNKGME 523 *****DIMER HELIX*****
CAA05410.2 3ERT	CLY DMKEK FV LP SW KVEK LG KV VE TL RT KE HR AE AS PQT 614 HL Y SM KCK KN V VP ---LYDLLLLEMLDAHRLHAP----- 552 ***

Figure 8: Genome Threader alignment (3ERT numbering corresponds to position in the full-length sequence rather than crystallised domain)

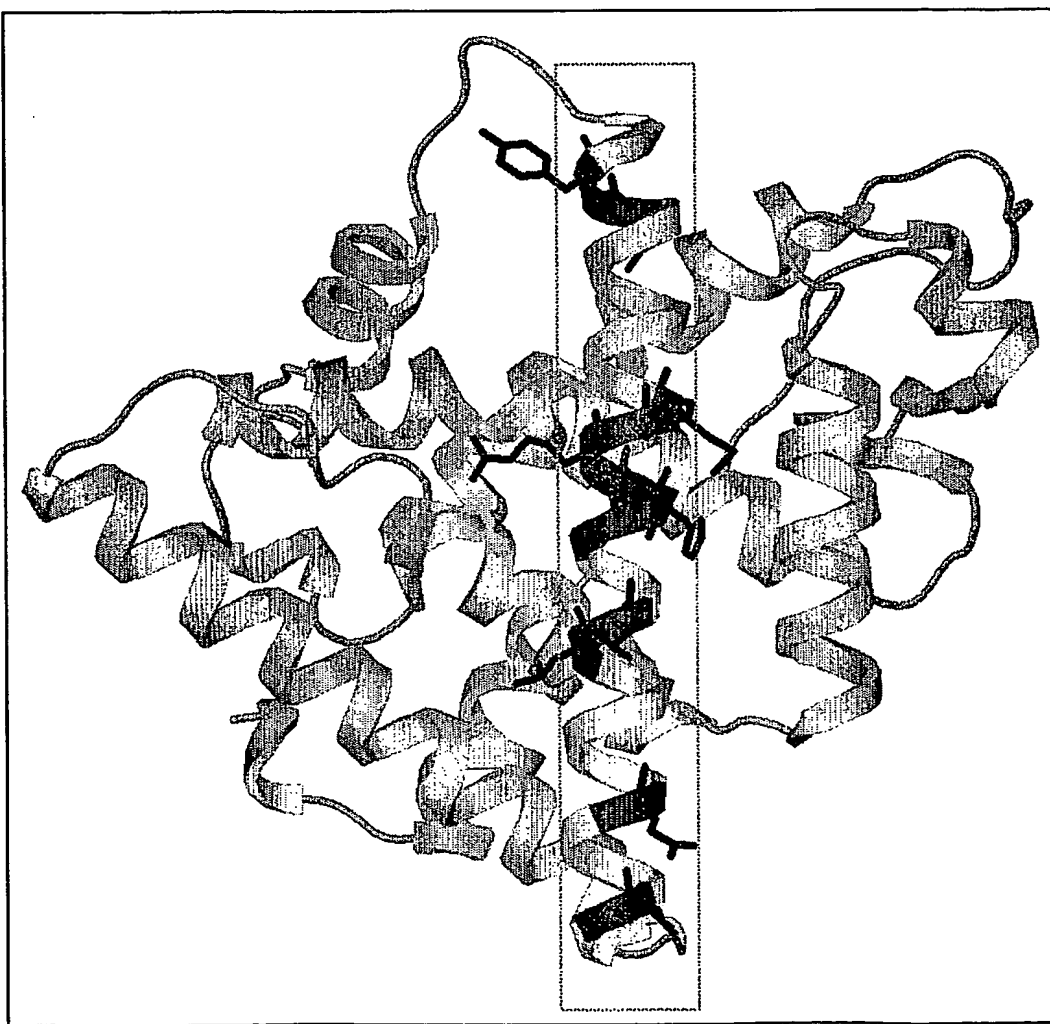


Figure 9: Dimerisation helix is enclosed in dotted box.

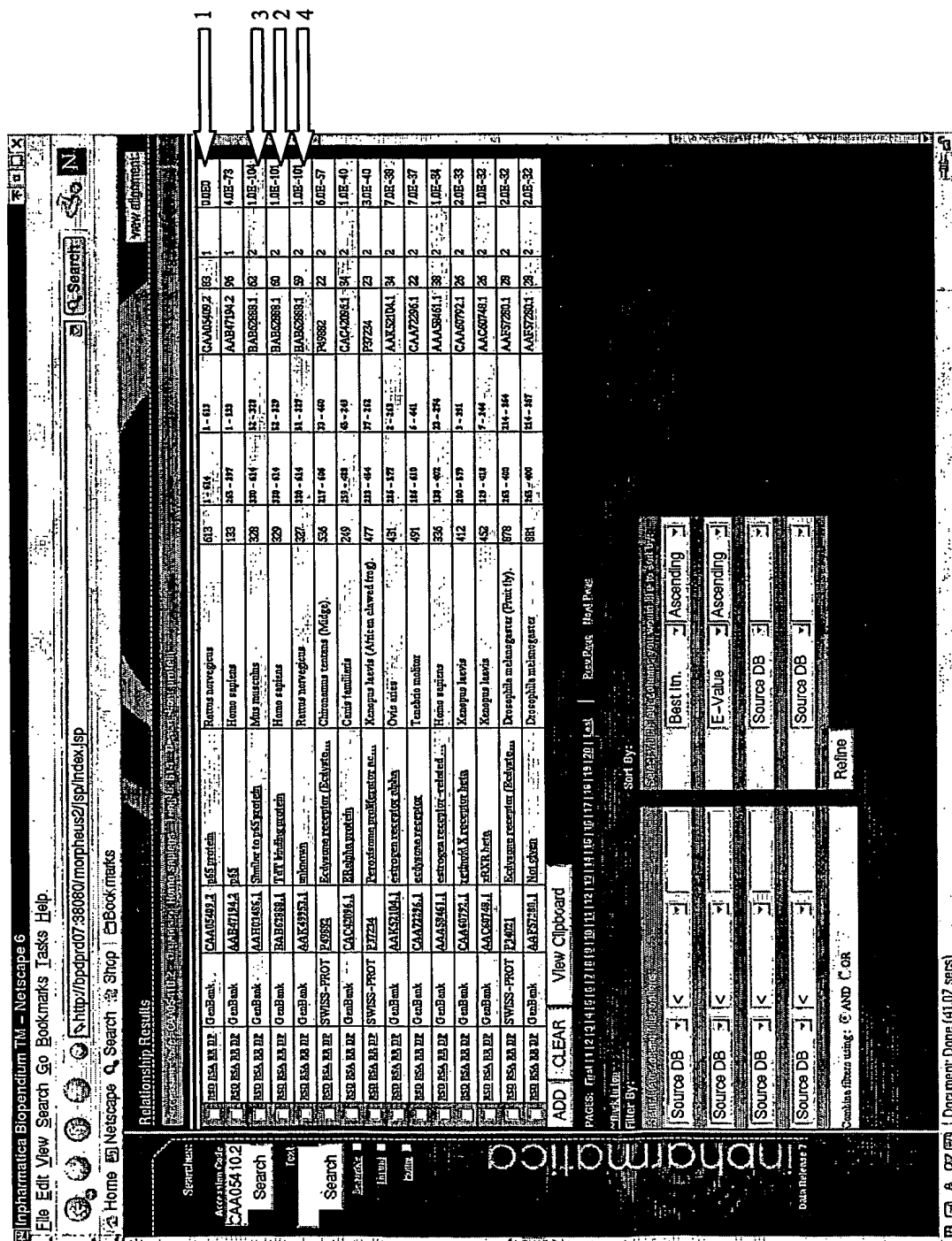


Figure 10

inpharmatica Biopendium TM - Netscape 6

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PAGES: First 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 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2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 264

[illegible]

3ERT	-----	MDPENVRAEGGDMREKVRLLSSARQ-RLRCSTKNSLLVARTC--VLRIVDWIEQDLKSTCE	57
CAA05409.2		MGPENESVPGGEMWGRVCVFSARQKRPRCSTLNSLLVARTCYNMLALVDWIEQDFKSTWR	60
3ERT	-----	KAHVSLRGYLDLQCCGRRRKEVAGA-LGGDTRDPKPKPRGGSKKNVEVYGGDDVGSQAADS	116
CAA05409.2		KAHVSLRGFLDFEL--GRRKEVAGAFLLGGDTRDPKPKPRGGSKKNVEVYDDDDVGSQAADS	118
3ERT	-----	PRKQLAAKGTFRDKDKIEALFKLGELVAKKALSSAITWFPNSVSPHHAHYGDEILYKDES	176
CAA05409.2		PGKRMAPKGTFRDKDKFEGLFKLGALVAKKALTAFSCSPNRGSPHHAHYGDEILYKVES	178
3ERT	-----	GLVNISEGGRGVEIHPPDNFGITLDEDLGFPQIIVINVKPQTEEANTWYRQDLKYHNS	236
CAA05409.2		GPVNICEGGRGVGIHPPDPNYG-DTLDENLGLPQKIVIKVKPQTEEANTWLRQDLKNHNS	237
3ERT	-----	ANEAGYSDENKTFVRGCRKDGHSERNMMTTGDRNSKKAQPVNFSLMASLALDSRGKAAGP	296
CAA05409.2		AKEAGGSDEIKTFVTGCKKDGHSGRKNMTTHDRNSKKWQVRVNLISMASLQLDSSRGGRAGE	297
3ERT	-----	RRGARRLCLVCEDYASCSNTCVWSCEAYKVFFRRSQSFTDPACFTNDCNISKNRSKSCPA	356
CAA05409.2		RRGARRLCLVCEDYASCSNTCVWSCEAYKVFFRRSQSFTDPACFTNDCNISKNRSKSCPA	357
3ERT	-----	CLLRLCLQPSINEIRKDKRAALNVRDNGVEEVDMTGPSWTCCLKLLFSDGKVIPLRLAHELP	416
CAA05409.2		CLLRLCLHPSINEIRKDKRAALKVRDNGVEEVDMTGPSWTCCLKLLFSDGKVIPLRLGHELP	417

Figure 13 Part I

3ERT
CAA05409.2
CAA05410.2
GLLTNIADREL VH-MINWAKRVPGFVDLTLLHDQVHLLLECAWLEILMIGLVWRSMEHPGKL 402
GIKGRQAEESHRGSPIPKKRKGWPPGHVLSNDRAAAGTVWPKSCPEPIRREGPKWDAR 476
GIKGRQAKQQSHRGSPIPKNRKGWPPGHVLSNDGAGGRVWKKKCKPIRREGPKWDR 477

3ERT
CAA05409.2
CAA05410.2
LFAPNLLDRNQKCVGMVEIFDMLLATSS--RFRMNLQGEFEVCLKSIILLNSGVYT 460
LN-----ESTTFVLGSRANKALGKGTRGRIYIKHPHLFKYAADPQD 518
LN-----ESTPLFWGSRANKSLGKGTRGRIFIKHPHLFKFAADPQD 519

3ERT
CAA05409.2
CAA05410.2
FLSSTLKSLEEKDHIHRVLDKITDTLIHLMAKAGLTLLQQHQRLAQLLILSHIRHMSNK 520
K-----HWLAEQQLHMRATGGK----MAYLLIEEDIE-QHHGQRFVAVFLKISHIRHMVEG 568
K-----HWLAEQQLHMRATGGK----MAYLLIEEDIG-QHHGQGFVPMLLKISHIRHMVGG 569
*****DIMER HELIX*****

3ERT
CAA05409.2
CAA05410.2
GMEHLYSMCKKNVVP---LYDLLLEMLDAHRLHAP----- 552
VAHCLYDMKVIQFVLPSWKVEKLRKYVETLRTENEHRAAEASPQT 613
VAHCLYDMKEKKFVLPSWKVEKLRKYVETLRTETEKEHRAAEASPQT 614

Figure 13 Part II

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http://srs.abl.ac.uk/srs6html.cgi-bin/wget?-id=9CQW1IURXC--e+InterProScan%27O5474S%27

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InterProScan

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Protein	Q5H745 OS:FRAS length: 613 aa;cds: 04457 DA:123027D	928-3697
InterPro	Zn-finger, C4-type serine/threonine (family)	928-3697
IPRO01628	PRODOM: P200055 Zn_finger	928-3697
	PFAM: PF00103 7-21	928-3697
	SMART: SM00393 Zn_finger	928-3697

SRS 613 | Feedback

Document Done (1925 sers)

Figure 14

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http://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi

2: Home Netscape Search Shop Bookmarks

CD-Search Enter 17

RPC-RAFT 2.2.2 [Dec-14-2001]
Query: Local sequence: gi14753887|emb|DAM05409.2| p65 protein
(Rattus norvegicus)
(613 letters)
Database: nr01's app. v1.54
3693 PSSMs; 716,011 total columns

Mouse-over boxes to display more information

1p 2p 3p 4p 5p 6p 7p 8p 9p 10p 11p 12p 13p 14p 15p 16p 17p 18p 19p 20p 21p 22p 23p 24p 25p 26p 27p 28p 29p 30p 31p 32p 33p 34p 35p 36p 37p 38p 39p 40p 41p 42p 43p 44p 45p 46p 47p 48p 49p 50p 51p 52p 53p 54p 55p 56p 57p 58p 59p 60p 61p 62p 63p 64p 65p 66p 67p 68p 69p 70p 71p 72p 73p 74p 75p 76p 77p 78p 79p 80p 81p 82p 83p 84p 85p 86p 87p 88p 89p 90p 91p 92p 93p 94p 95p 96p 97p 98p 99p 100p 101p 102p 103p 104p 105p 106p 107p 108p 109p 110p 111p 112p 113p 114p 115p 116p 117p 118p 119p 120p 121p 122p 123p 124p 125p 126p 127p 128p 129p 130p 131p 132p 133p 134p 135p 136p 137p 138p 139p 140p 141p 142p 143p 144p 145p 146p 147p 148p 149p 150p 151p 152p 153p 154p 155p 156p 157p 158p 159p 160p 161p 162p 163p 164p 165p 166p 167p 168p 169p 170p 171p 172p 173p 174p 175p 176p 177p 178p 179p 180p 181p 182p 183p 184p 185p 186p 187p 188p 189p 190p 191p 192p 193p 194p 195p 196p 197p 198p 199p 200p 201p 202p 203p 204p 205p 206p 207p 208p 209p 210p 211p 212p 213p 214p 215p 216p 217p 218p 219p 220p 221p 222p 223p 224p 225p 226p 227p 228p 229p 230p 231p 232p 233p 234p 235p 236p 237p 238p 239p 240p 241p 242p 243p 244p 245p 246p 247p 248p 249p 250p 251p 252p 253p 254p 255p 256p 257p 258p 259p 260p 261p 262p 263p 264p 265p 266p 267p 268p 269p 270p 271p 272p 273p 274p 275p 276p 277p 278p 279p 280p 281p 282p 283p 284p 285p 286p 287p 288p 289p 290p 291p 292p 293p 294p 295p 296p 297p 298p 299p 300p 301p 302p 303p 304p 305p 306p 307p 308p 309p 310p 311p 312p 313p 314p 315p 316p 317p 318p 319p 320p 321p 322p 323p 324p 325p 326p 327p 328p 329p 330p 331p 332p 333p 334p 335p 336p 337p 338p 339p 340p 341p 342p 343p 344p 345p 346p 347p 348p 349p 350p 351p 352p 353p 354p 355p 356p 357p 358p 359p 360p 361p 362p 363p 364p 365p 366p 367p 368p 369p 370p 371p 372p 373p 374p 375p 376p 377p 378p 379p 380p 381p 382p 383p 384p 385p 386p 387p 388p 389p 390p 391p 392p 393p 394p 395p 396p 397p 398p 399p 400p 401p 402p 403p 404p 405p 406p 407p 408p 409p 410p 411p 412p 413p 414p 415p 416p 417p 418p 419p 420p 421p 422p 423p 424p 425p 426p 427p 428p 429p 430p 431p 432p 433p 434p 435p 436p 437p 438p 439p 440p 441p 442p 443p 444p 445p 446p 447p 448p 449p 450p 451p 452p 453p 454p 455p 456p 457p 458p 459p 460p 461p 462p 463p 464p 465p 466p 467p 468p 469p 470p 471p 472p 473p 474p 475p 476p 477p 478p 479p 480p 481p 482p 483p 484p 485p 486p 487p 488p 489p 490p 491p 492p 493p 494p 495p 496p 497p 498p 499p 500p 501p 502p 503p 504p 505p 506p 507p 508p 509p 510p 511p 512p 513p 514p 515p 516p 517p 518p 519p 520p 521p 522p 523p 524p 525p 526p 527p 528p 529p 530p 531p 532p 533p 534p 535p 536p 537p 538p 539p 540p 541p 542p 543p 544p 545p 546p 547p 548p 549p 550p 551p 552p 553p 554p 555p 556p 557p 558p 559p 560p 561p 562p 563p 564p 565p 566p 567p 568p 569p 570p 571p 572p 573p 574p 575p 576p 577p 578p 579p 580p 581p 582p 583p 584p 585p 586p 587p 588p 589p 590p 591p 592p 593p 594p 595p 596p 597p 598p 599p 600p 601p 602p 603p 604p 605p 606p 607p 608p 609p 610p 611p 612p 613p 614p 615p 616p 617p 618p 619p 620p 621p 622p 623p 624p 625p 626p 627p 628p 629p 630p 631p 632p 633p 634p 635p 636p 637p 638p 639p 640p 641p 642p 643p 644p 645p 646p 647p 648p 649p 650p 651p 652p 653p 654p 655p 656p 657p 658p 659p 660p 661p 662p 663p 664p 665p 666p 667p 668p 669p 670p 671p 672p 673p 674p 675p 676p 677p 678p 679p 680p 681p 682p 683p 684p 685p 686p 687p 688p 689p 690p 691p 692p 693p 694p 695p 696p 697p 698p 699p 700p 701p 702p 703p 704p 705p 706p 707p 708p 709p 710p 711p 712p 713p 714p 715p 716p 717p 718p 719p 720p 721p 722p 723p 724p 725p 726p 727p 728p 729p 730p 731p 732p 733p 734p 735p 736p 737p 738p 739p 740p 741p 742p 743p 744p 745p 746p 747p 748p 749p 750p 751p 752p 753p 754p 755p 756p 757p 758p 759p 760p 761p 762p 763p 764p 765p 766p 767p 768p 769p 770p 771p 772p 773p 774p 775p 776p 777p 778p 779p 780p 781p 782p 783p 784p 785p 786p 787p 788p 789p 790p 791p 792p 793p 794p 795p 796p 797p 798p 799p 800p 801p 802p 803p 804p 805p 806p 807p 808p 809p 810p 811p 812p 813p 814p 815p 816p 817p 818p 819p 820p 821p 822p 823p 824p 825p 826p 827p 828p 829p 830p 831p 832p 833p 834p 835p 836p 837p 838p 839p 840p 841p 842p 843p 844p 845p 846p 847p 848p 849p 850p 851p 852p 853p 854p 855p 856p 857p 858p 859p 860p 861p 862p 863p 864p 865p 866p 867p 868p 869p 870p 871p 872p 873p 874p 875p 876p 877p 878p 879p 880p 881p 882p 883p 884p 885p 886p 887p 888p 889p 890p 891p 892p 893p 894p 895p 896p 897p 898p 899p 900p 901p 902p 903p 904p 905p 906p 907p 908p 909p 910p 911p 912p 913p 914p 915p 916p 917p 918p 919p 920p 921p 922p 923p 924p 925p 926p 927p 928p 929p 930p 931p 932p 933p 934p 935p 936p 937p 938p 939p 940p 941p 942p 943p 944p 945p 946p 947p 948p 949p 950p 951p 952p 953p 954p 955p 956p 957p 958p 959p 960p 961p 962p 963p 964p 965p 966p 967p 968p 969p 970p 971p 972p 973p 974p 975p 976p 977p 978p 979p 980p 981p 982p 983p 984p 985p 986p 987p 988p 989p 990p 991p 992p 993p 994p 995p 996p 997p 998p 999p 1000p 1001p 1002p 1003p 1004p 1005p 1006p 1007p 1008p 1009p 1010p 1011p 1012p 1013p 1014p 1015p 1016p 1017p 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1184p 1185p 1186p 1187p 1188p 1189p 1190p 1191p 1192p 1193p 1194p 1195p 1196p 1197p 1198p 1199p 1200p 1201p 1202p 1203p 1204p 1205p 1206p 1207p 1208p 1209p 1210p 1211p 1212p 1213p 1214p 1215p 1216p 1217p 1218p 1219p 1220p 1221p 1222p 1223p 1224p 1225p 1226p 1227p 1228p 1229p 1230p 1231p 1232p 1233p 1234p 1235p 1236p 1237p 1238p 1239p 1240p 1241p 1242p 1243p 1244p 1245p 1246p 1247p 1248p 1249p 1250p 1251p 1252p 1253p 1254p 1255p 1256p 1257p 1258p 1259p 1260p 1261p 1262p 1263p 1264p 1265p 1266p 1267p 1268p 1269p 1270p 1271p 1272p 1273p 1274p 1275p 1276p 1277p 1278p 1279p 1280p 1281p 1282p 1283p 1284p 1285p 1286p 1287p 1288p 1289p 1290p 1291p 1292p 1293p 1294p 1295p 1296p 1297p 1298p 1299p 1300p 1301p 1302p 1303p 1304p 1305p 1306p 1307p 1308p 1309p 1310p 1311p 1312p 1313p 1314p 1315p 1316p 1317p 1318p 1319p 1320p 1321p 1322p 1323p 1324p 1325p 1326p 1327p 1328p 1329p 1330p 1331p 1332p 1333p 1334p 1335p 1336p 1337p 1338p 1339p 1340p 1341p 1342p 1343p 1344p 1345p 1346p 1347p 1348p 1349p 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1516p 1517p 1518p 1519p 1520p 1521p 1522p 1523p 1524p 1525p 1526p 1527p 1528p 1529p 1530p 1531p 1532p 1533p 1534p 1535p 1536p 1537p 1538p 1539p 1540p 1541p 1542p 1543p 1544p 1545p 1546p 1547p 1548p 1549p 1550p 1551p 1552p 1553p 1554p 1555p 1556p 1557p 1558p 1559p 1560p 1561p 1562p 1563p 1564p 1565p 1566p 1567p 1568p 1569p 1570p 1571p 1572p 1573p 1574p 1575p 1576p 1577p 1578p 1579p 1580p 1581p 1582p 1583p 1584p 1585p 1586p 1587p 1588p 1589p 1590p 1591p 1592p 1593p 1594p 1595p 1596p 1597p 1598p 1599p 1600p 1601p 1602p 1603p 1604p 1605p 1606p 1607p 1608p 1609p 1610p 1611p 1612p 1613p 1614p 1615p 1616p 1617p 1618p 1619p 1620p 1621p 1622p 1623p 1624p 1625p 1626p 1627p 1628p 1629p 1630p 1631p 1632p 1633p 1634p 1635p 1636p 1637p 1638p 1639p 1640p 1641p 1642p 1643p 1644p 1645p 1646p 1647p 1648p 1649p 1650p 1651p 1652p 1653p 1654p 1655p 1656p 1657p 1658p 1659p 1660p 1661p 1662p 1663p 1664p 1665p 1666p 1667p 1668p 1669p 1670p 1671p 1672p 1673p 1674p 1675p 1676p 1677p 1678p 1679p 1680p 1681p 1682p 1683p 1684p 1685p 1686p 1687p 1688p 1689p 1690p 1691p 1692p 1693p 1694p 1695p 1696p 1697p 1698p 1699p 1700p 1701p 1702p 1703p 1704p 1705p 1706p 1707p 1708p 1709p 1710p 1711p 1712p 1713p 1714p 1715p 1716p 1717p 1718p 1719p 1720p 1721p 1722p 1723p 1724p 1725p 1726p 1727p 1728p 1729p 1730p 1731p 1732p 1733p 1734p 1735p 1736p 1737p 1738p 1739p 1740p 1741p 1742p 1743p 1744p 1745p 1746p 1747p 1748p 1749p 1750p 1751p 1752p 1753p 1754p 1755p 1756p 1757p 1758p 1759p 1760p 1761p 1762p 1763p 1764p 1765p 1766p 1767p 1768p 1769p 1770p 1771p 1772p 1773p 1774p 1775p 1776p 1777p 1778p 1779p 1780p 1781p 1782p 1783p 1784p 1785p 1786p 1787p 1788p 1789p 1790p 1791p 1792p 1793p 1794p 1795p 1796p 1797p 1798p 1799p 1800p 1801p 1802p 1803p 1804p 1805p 1806p 1807p 1808p 1809p 1810p 1811p 1812p 1813p 1814p 1815p 1816p 1817p 1818p 1819p 1820p 1821p 1822p 1823p 1824p 1825p 1826p 1827p 1828p 1829p 1830p 1831p 1832p 1833p 1834p 1835p 1836p 1837p 1838p 1839p 1840p 1841p 1842p 1843p 1844p 1845p 1846p 1847p 1848p 1849p 1850p 1851p 1852p 1853p 1854p 1855p 1856p 1857p 1858p 1859p 1860p 1861p 1862p 1863p 1864p 1865p 1866p 1867p 1868p 1869p 1870p 1871p 1872p 1873p 1874p 1875p 1876p 1877p 1878p 1879p 1880p 1881p 1882p 1883p 1884p 1885p 1886p 1887p 1888p 1889p 1890p 1891p 1892p 1893p 1894p 1895p 1896p 1897p 1898p 1899p 1900p 1901p 1902p 1903p 1904p 1905p 1906p 1907p 1908p 1909p 1910p 1911p 1912p 1913p 1914p 1915p 1916p 1917p 1918p 1919p 1920p 1921p 1922p 1923p 1924p 1925p 1926p 1927p 1928p 1929p 1930p 1931p 1932p 1933p 1934p 1935p 1936p 1937p 1938p 1939p 1940p 1941p 1942p 1943p 1944p 1945p 1946p 1947p 1948p 1949p 1950p 1951p 1952p 1953p 1954p 1955p 1956p 1957p 1958p 1959p 1960p 1961p 1962p 1963p 1964p 1965p 1966p 1967p 1968p 1969p 1970p 1971p 1972p 1973p 1974p 1975p 1976p 1977p 1978p 1979p 1980p 1981p 1982p 1983p 1984p 1985p 1986p 1987p 1988p 1989p 1990p 1991p 1992p 1993p 1994p 1995p 1996p 1997p 1998p 1999p 2000p 2001p 2002p 2003p 2004p 2005p 2006p 2007p 2008p 2009p 2010p 2011p 2012p 2013p 2014p 2015p 2016p 2017p 2018p 2019p 2020p 2021p 2022p 2023p 2024p 2025p 2026p 2027p 2028p 2029p 2030p 2031p 2032p 2033p 2034p 2035p 2036p 2037p 2038p 2039p 2040p 2041p 2042p 2043p 2044p 2045p 2046p 2047p 2048p 2049p 2050p 2051p 2052p 2053p 2054p 2055p 2056p 2057p 2058p 2059p 2060p 2061p 2062p 2063p 2064p 2065p 2066p 2067p 2068p 2069p 2070p 2071p 2072p 2073p 2074p 2075p 2076p 2077p 2078p 2079p 2080p 2081p 2082p 2083p 2084p 2085p 2086p 2087p 2088p 2089p 2090p 2091p 2092p 2093p 2094p 2095p 2096p 2097p 2098p 2099p 2100p 2101p 2102p 2103p 2104p 2105p 2106p 2107p 2108p 2109p 2110p 2111p 2112p 2113p 2114p 2115p 2116p 2117p 2118p 2119p 2120p 2121p 2122p 2123p 2124p 2125p 2126p 2127p 2128p 2129p 2130p 2131p 2132p 2133p 2134p 2135p 2136p 2137p 2138p 2139p 2140p 2141p 2142p 2143p 2144p 2145p 2146p 2147p 2148p 2149p 2150p 2151p 2152p 2153p 2154p 2155p 2156p 2157p 2158p 2159p 2160p 2161p 2162p 2163p 2164p 2165p 2166p 2167p 2168p 2169p 2170p 2171p 2172p 2173p 2174p 2175p 2176p 2177p 2178p 2179p 2180p 2181p 2182p 2183p 2184p 2185p 2186p 2187p 2188p 2189p 219

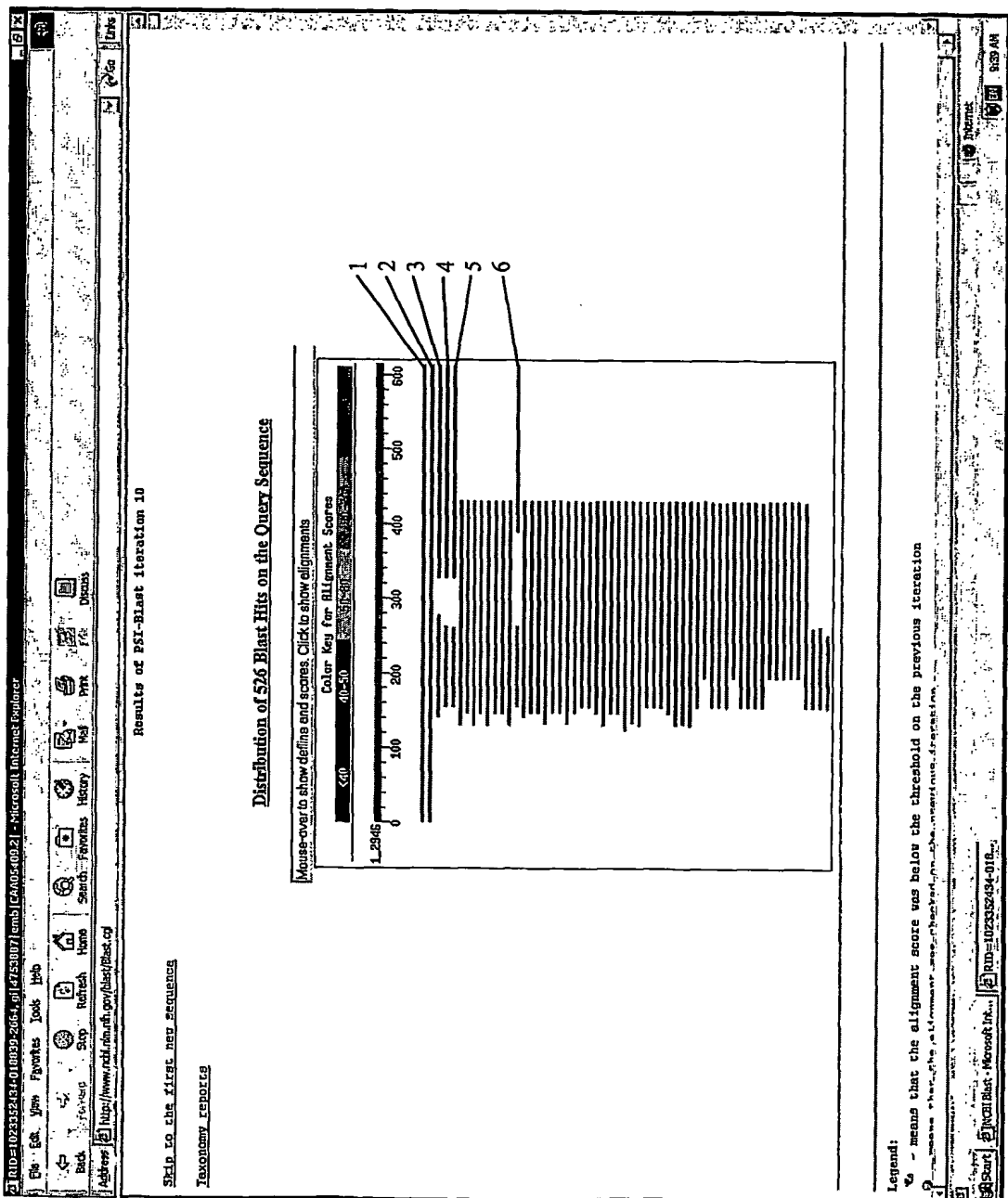
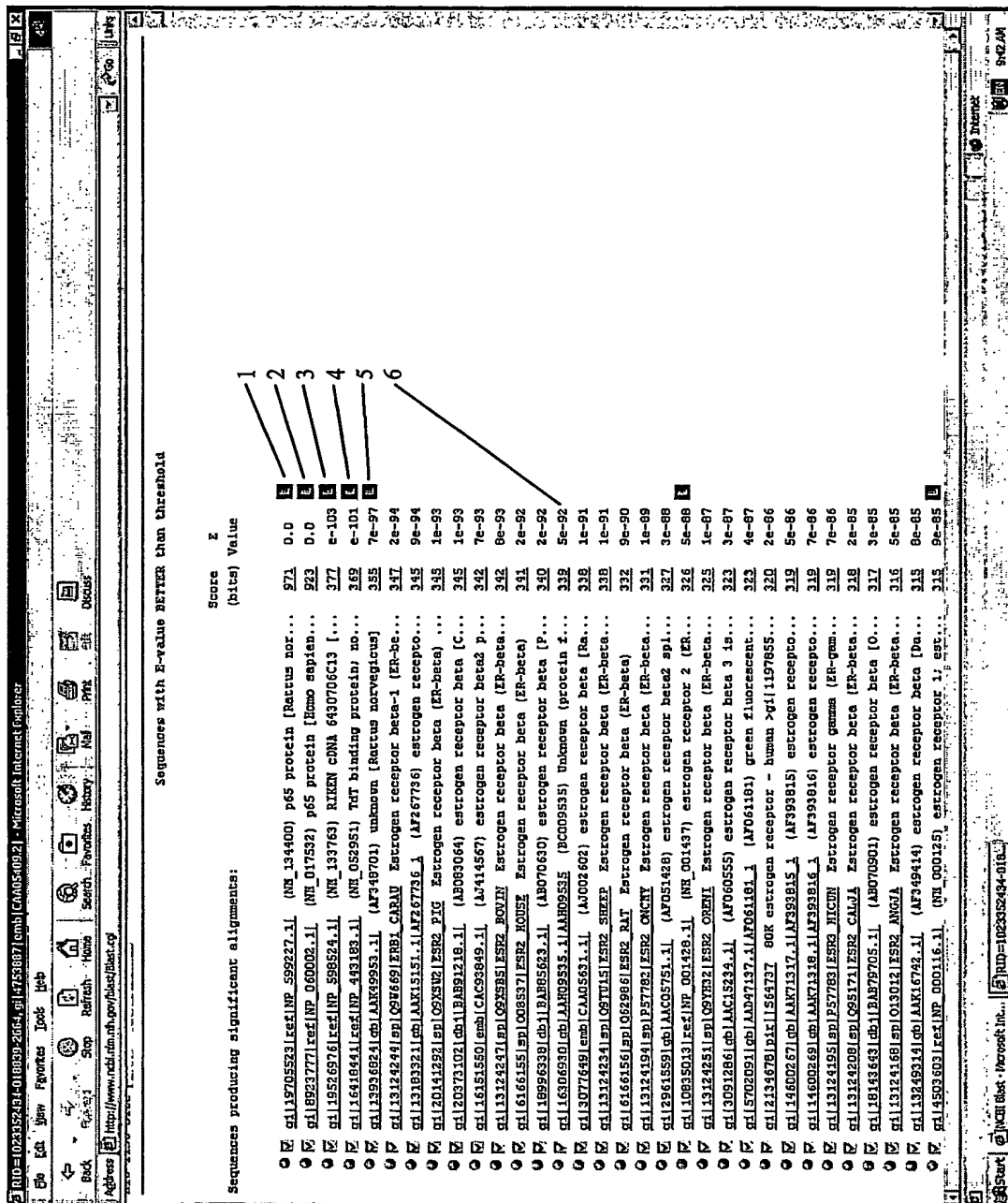


Figure 16A



[illegible]

Figure 17

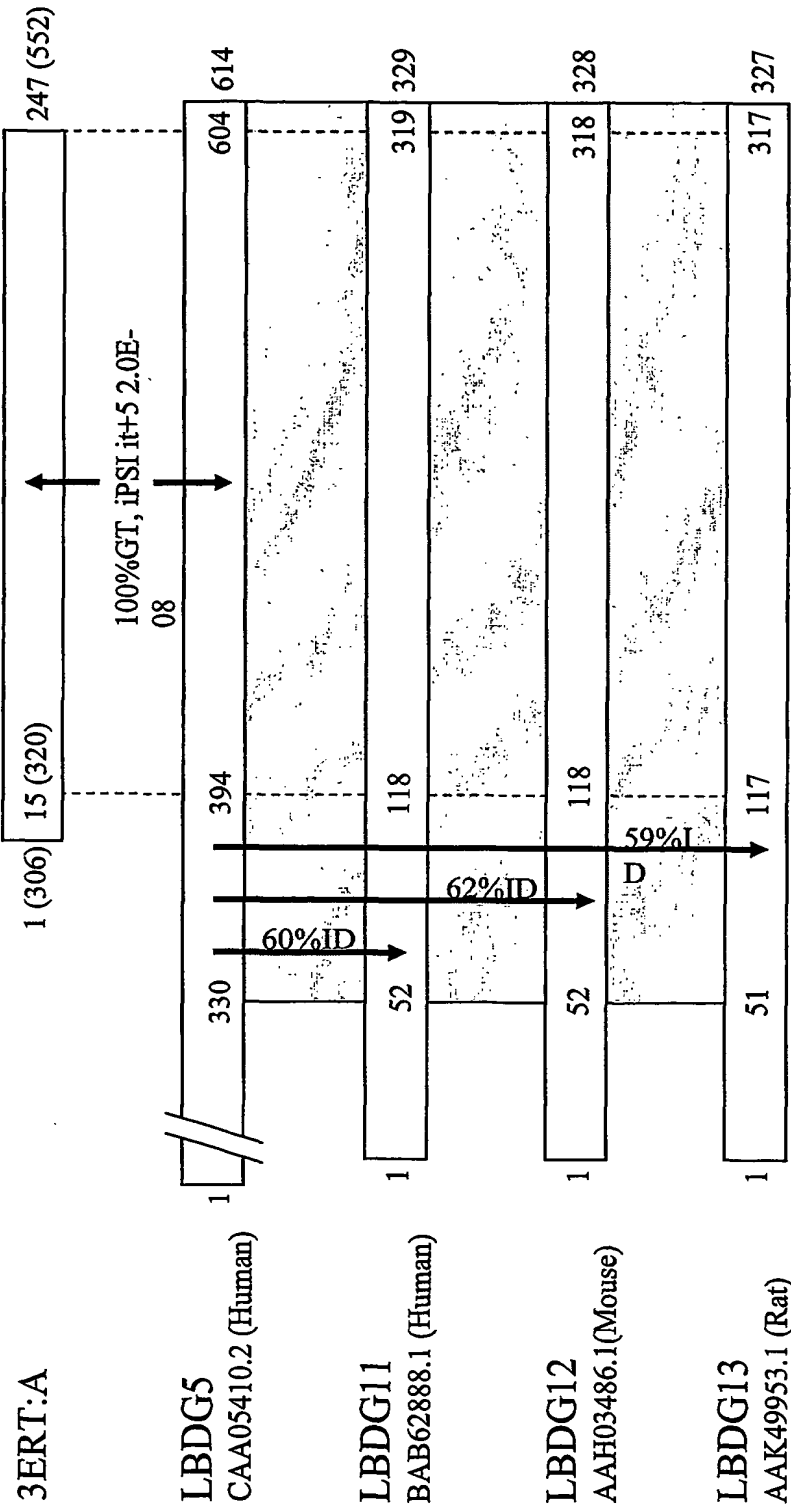


Figure 18: relationships between 3ERT:A, CAA05410.2 (LBDG5), BAB62888.1 (LBDG11), AAH03486.1 (LBDG12) and AAK49953.1 (LBDG13).

3ERT			MIGLVRSMEHPG-KLLFAPNLLLDNRNQGKCVGEMVEIFDMLLATSS--RFRMNLQEE	444
CAA05410.2	(LBDG5)		SCKPIRREGPKWW-DRLN-----ESTPLFWGSRANKSLGKGGRGRI	503
BAB62888.1	(LBDG11)		SCEPIRREGPKWDPARLN-----ESTTFLGSRANKALGMGGTRGRI	232
AAH03486.1	(LBDG12)		SCEPIRREGPKWDPARLN-----ESTTFLGSRANKALGMGGTRGRI	231
AAK49953.1	(LBDG13)		SCEPIRREGPKWDPARLN-----ESTTFLGSRANKALGMGGTRGRI	230
3ERT			FVCLKSIILNSGVYTFLSSTLKSLEEKDHIHRVLDKITDTLIHLMKAGLTQQQHQL	504
CAA05410.2	(LBDG5)		FIKHPHLFKFAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIG-QHHGQGF	553
BAB62888.1	(LBDG11)		YIKHPHLFKYAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIR-D-----	276
AAH03486.1	(LBDG12)		YIKHPHLFKYAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIR-D-----	275
AAK49953.1	(LBDG13)		YIKHPHLFKYAADPQDK-----HWLAEQHHMRATGGK---MAYLLIEEDIR-D-----	274
3ERT			AQLLLILSHIRHMSNKGMEHLYSMK---CKNVVP---LYDLLLEMLDAHRLHAP	552
CAA05410.2	(LBDG5)		PVMLLKISHIRHVMVGVAHCLYDMK---EKKFVLPSWKVEKIGKYVETLRTKEHRAAEA	610
BAB62888.1	(LBDG11)		---LAASDDYR-----GCL-DLKEELKSFVLPSSWVEKMRKYMETLRTENEHRAVEA	325
AAH03486.1	(LBDG12)		---LAASDDYR-----GCL-DLKEELKSFVLPSSWVEKMRKYMETLRTENEHRAVEA	324
AAK49953.1	(LBDG13)		---LAASDDYR-----GCL-DLKEELKSFVLPSSWVEKMRKYMETLRTENEHRAVEA	323
3ERT			----	552
CAA05410.2	(LBDG5)		SPQT	614
BAB62888.1	(LBDG11)		PPQT	329
AAH03486.1	(LBDG12)		PPQT	328
AAK49953.1	(LBDG13)		TPQT	327

Figure 19 PartII

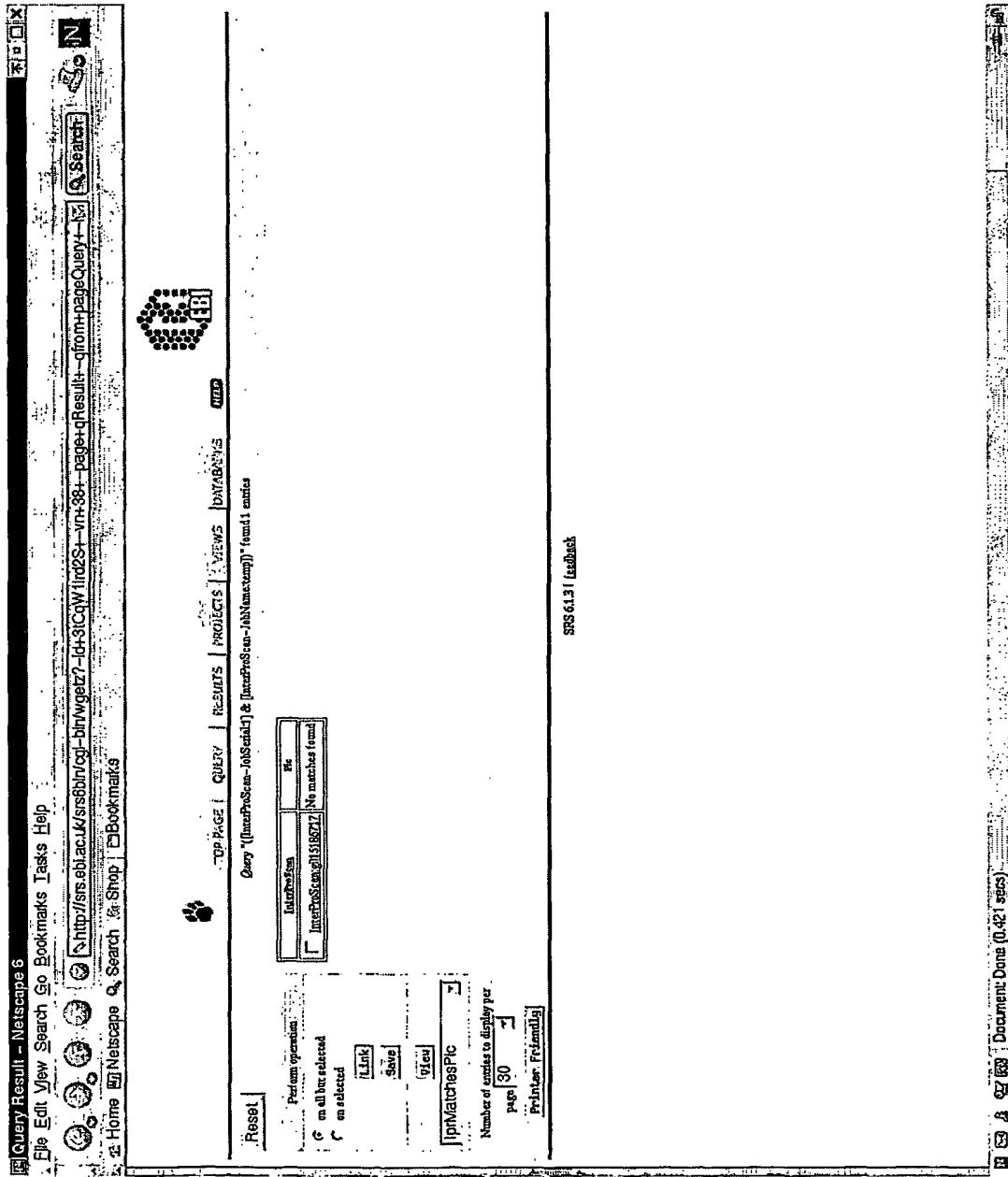


Figure 20

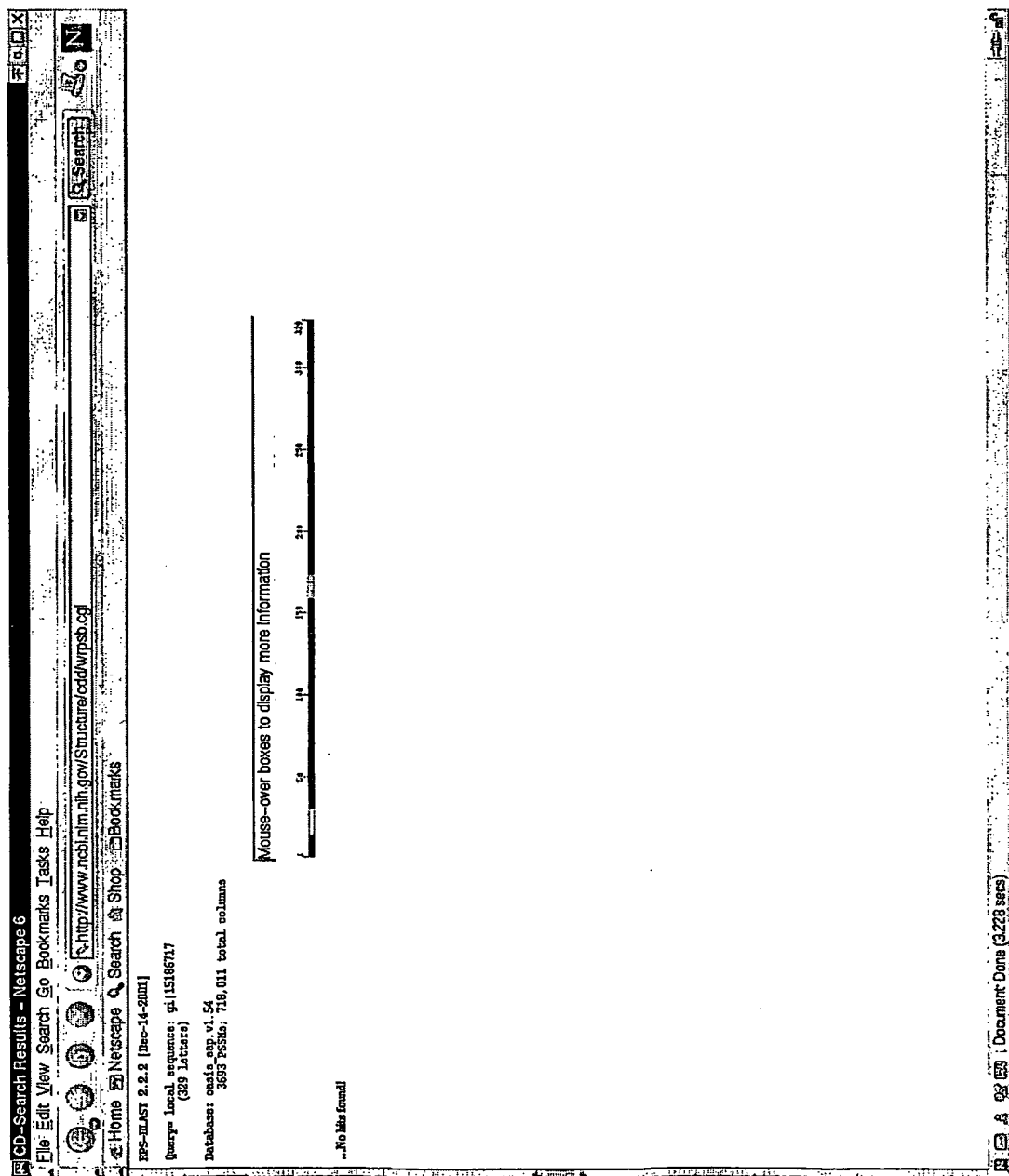


Figure 21

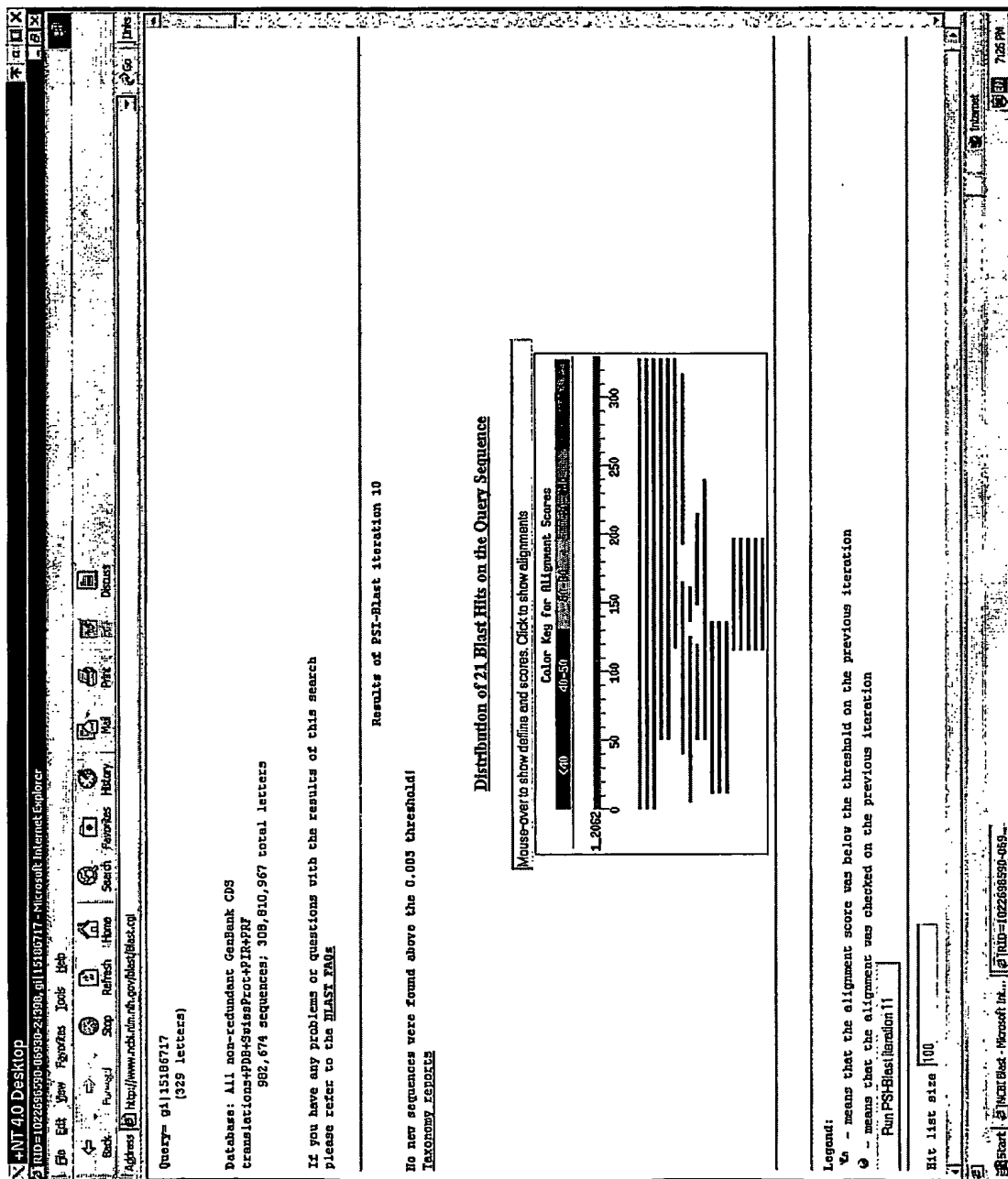


Figure 22

NT 4.0 Desktop
RID=102209590-06950-24990.gil15100717 - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Address http://www.ncbi.nlm.nih.gov/blast/...
Back Forward Stop Refresh Home Search Favorites History Mail Print
Run PSI-Blast iteration 11

Hit list size 100

Sequences producing significant alignments:

	Score	E
	(bits)	Value
gi116410441 ref NP_443183.1 (NM_052951) Tat binding protein no...	612	e-174
gi119526976 ref NP_598524.1 (NM_133763) RIKEN cDNA 643070G13 [...]	606	e-173
gi113936824 emb AA04953.1 (AF348701) unknown (Bartus norvegicus)	586	e-167
gi119705523 ref NP_599227.1 (NM_134400) p65 protein [Rattus nor...	428	e-119
gi118923771 ref NP_060002.1 (NM_017532) p65 protein [Homo sapien...	412	e-114
gi116906930 emb AA09595.1 AA09595 (BC009535) Unknown protein f...	397	e-110
gi111465987 emb CAC17442.1 (AL050348) ad447F3.4.2 (novel protei...	235	3e-61
gi113559866 emb CAC36107.1 (AL050348) ad447F3.4.3 (novel protei...	225	6e-58
gi117922271 emb AA047676.1 (AB003475) C01248 gene product [Drosop...	190	2e-47
gi119790342 emb AA047194.2 (S82307) p65 [Homo sapiens]	85	1e-15

Sequences with E-value WORSE than threshold

Run PSI-Blast iteration 11

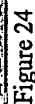
Sequences with E-value WORSE than threshold

gi117555590 ref NP_499042.1 (NM_066641) T2305.6.p [Caenorhabdit...	41	0.023
gi119256911 emb AA06997.1 AC005292.6 (AC005292) F26724.8 [Arabido...	38	0.14
gi118220680 ref NP_173737.1 (NM_102172) conserved hypothetical ...	38	0.14
gi118229951 emb AA06663.1 (AC002311) hypothetical protein [Arabi...	38	0.19
gi117026228 emb CAC65682.1 (AJ305314) ADAMTS-13 protein [Homo s...	34	2.1
gi117148513 emb CA012729.1 (AJ420810) ADAMTS-13 protein, varian...	34	2.6
gi118571521 ref XP_008414.1 (X088414) a disintegrin-like end ...	34	2.7
gi115963593 emb AA11095.1 AF414401.1 (AF414401) ADAMTS13 [Homo s...	34	2.8
gi117148515 emb CA012730.1 (AJ420811) ADAMTS-13 protein, trunca...	34	3.0
gi115888941 ref NP_354622.1 (NC_003062) ACR_C_3005p [Agrobacter...	33	5.6
gi118225511 ref NP_080605.1 (NM_018193) mitochondrial ribosomal ...	32	6.1

Run PSI-Blast iteration 11

US Govt - NCBI Blast - Microsoft IE...

Figure 23



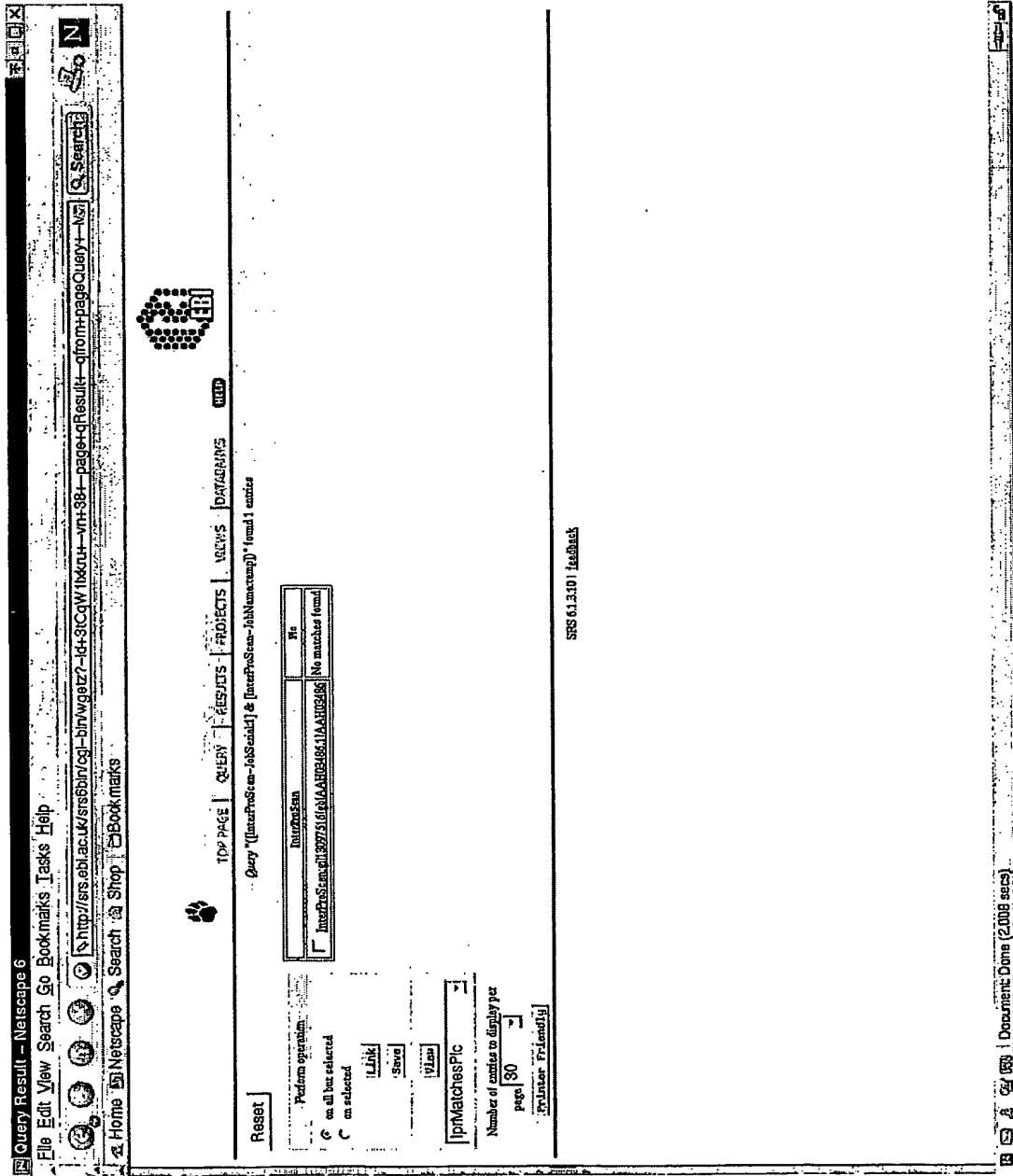


Figure 25

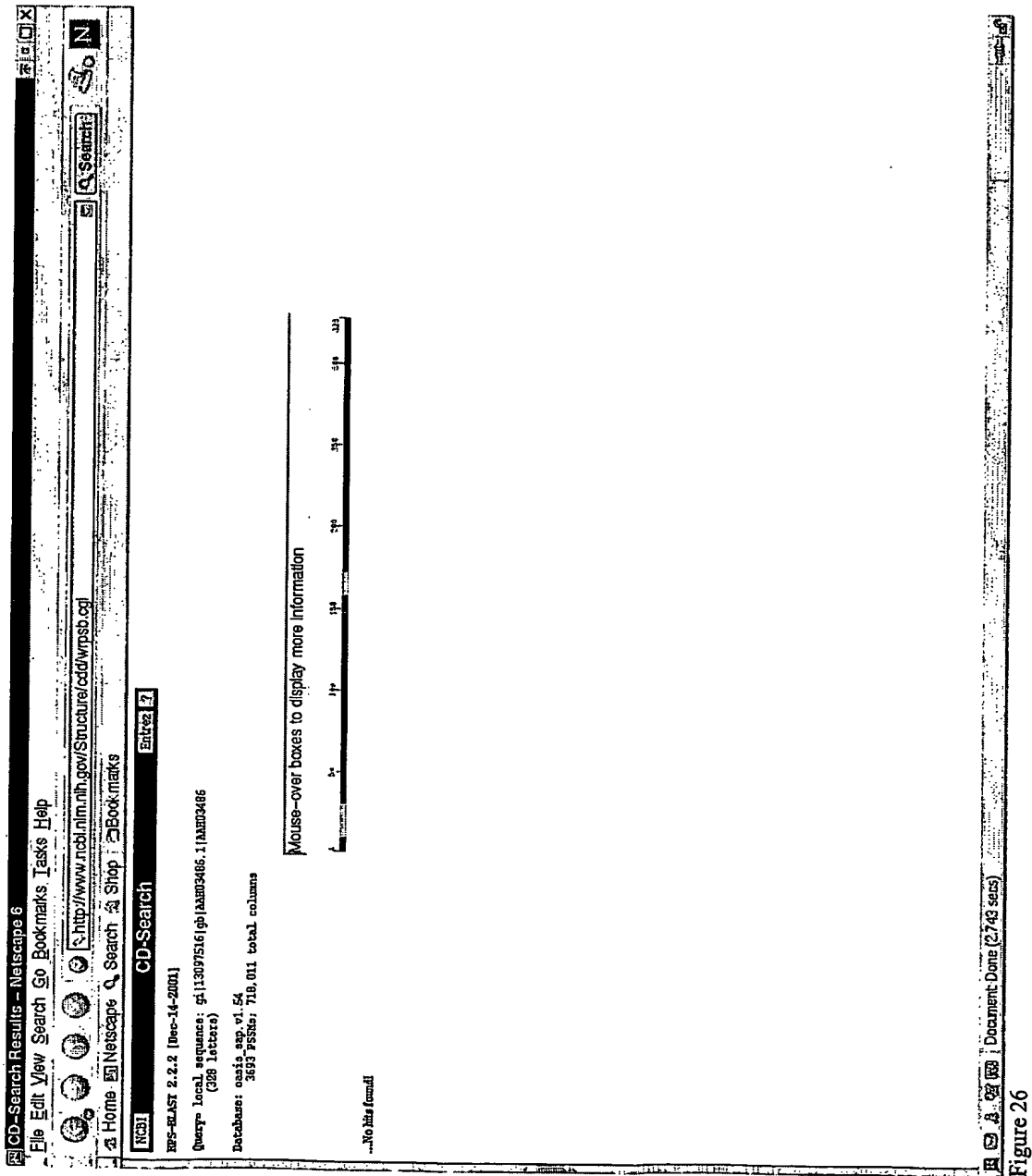


Figure 26

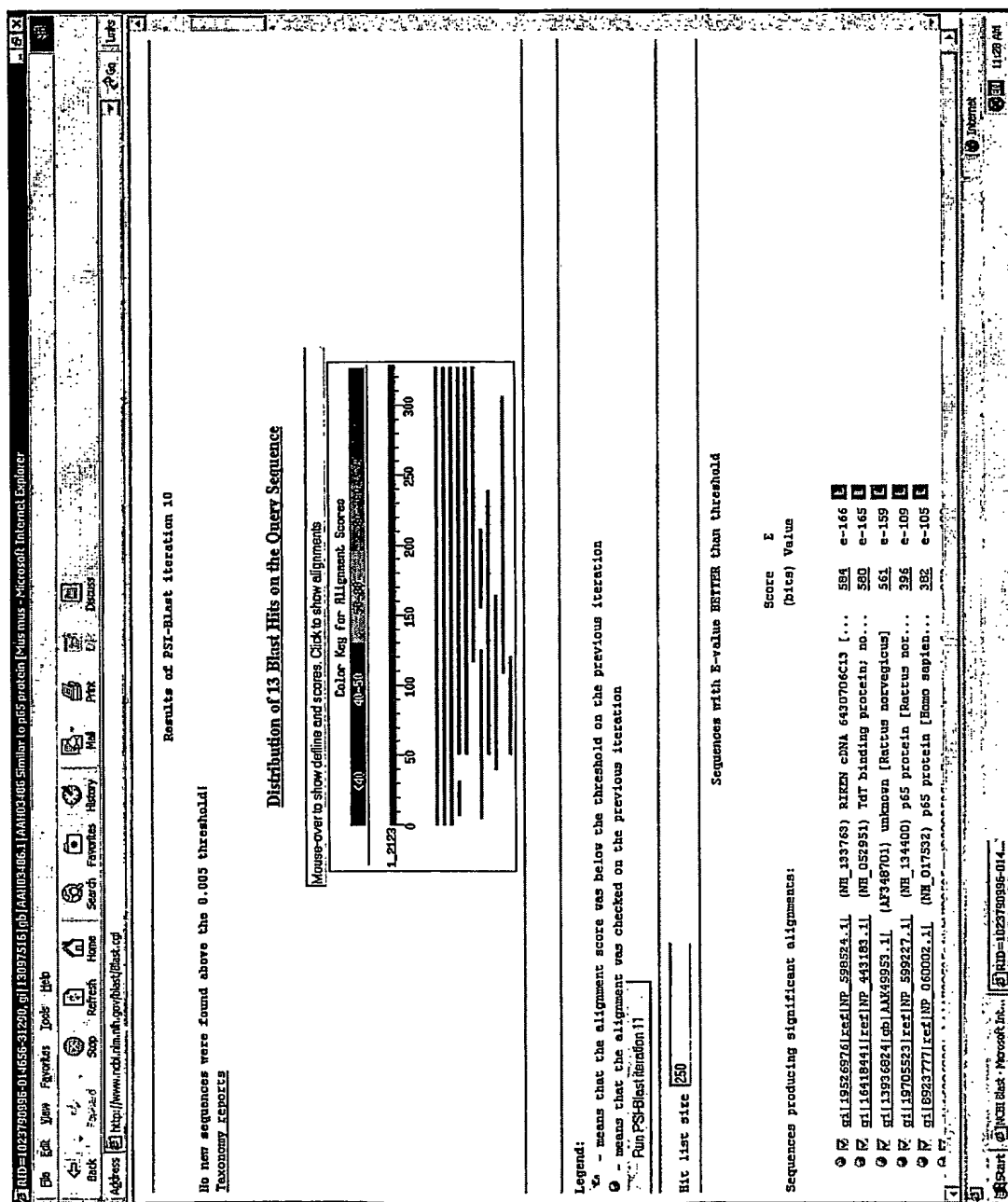


Figure 27

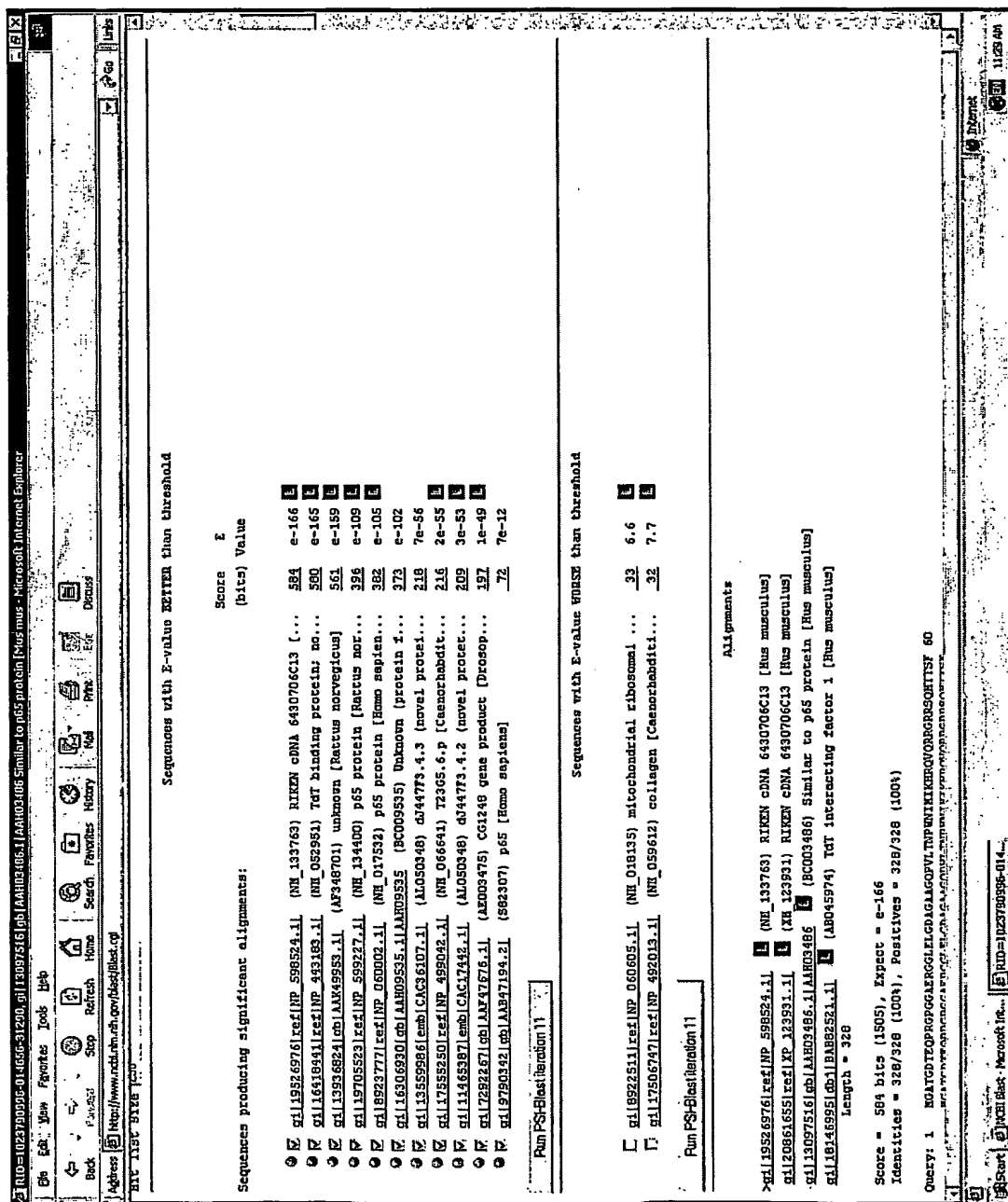
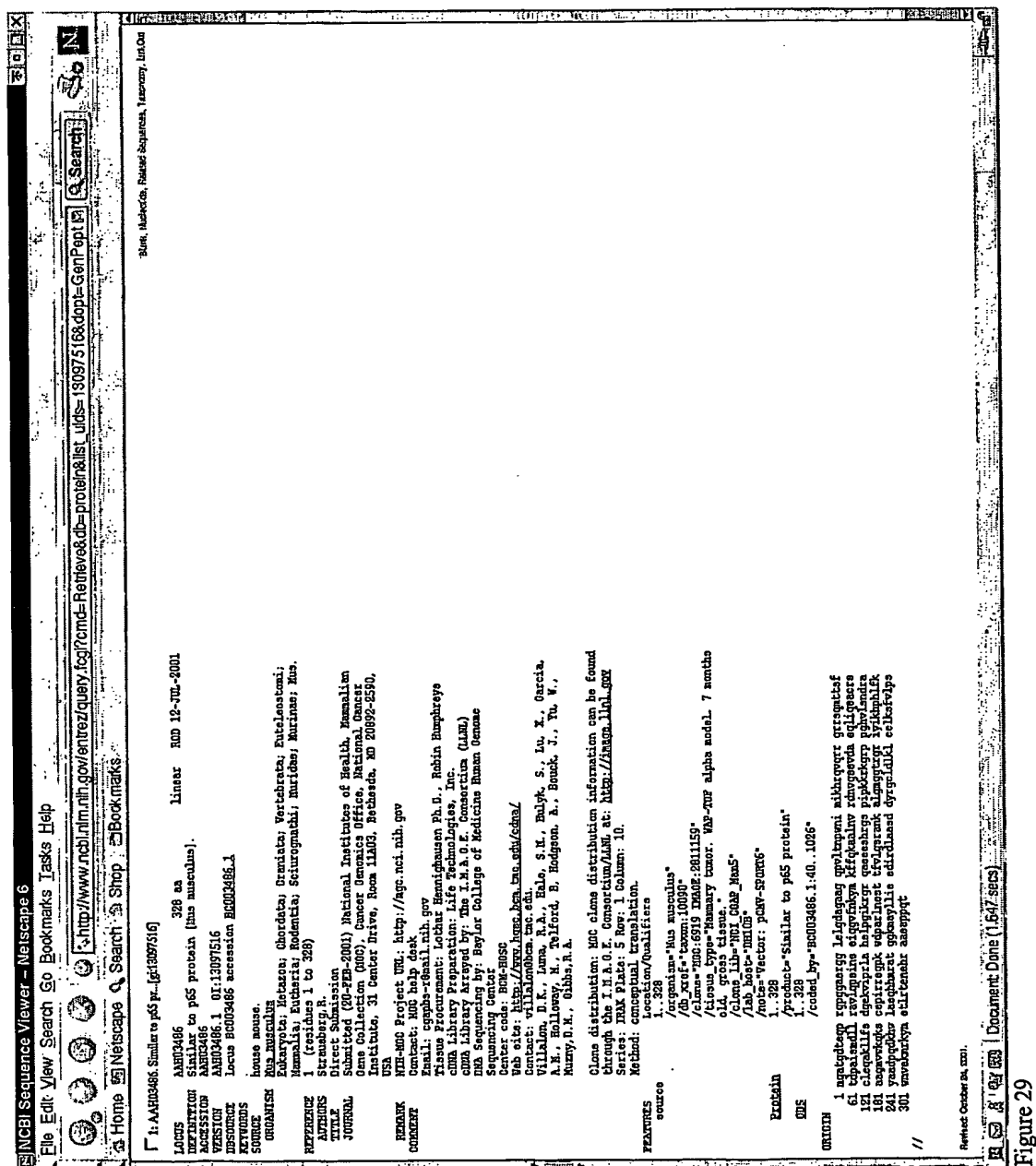


Figure 28



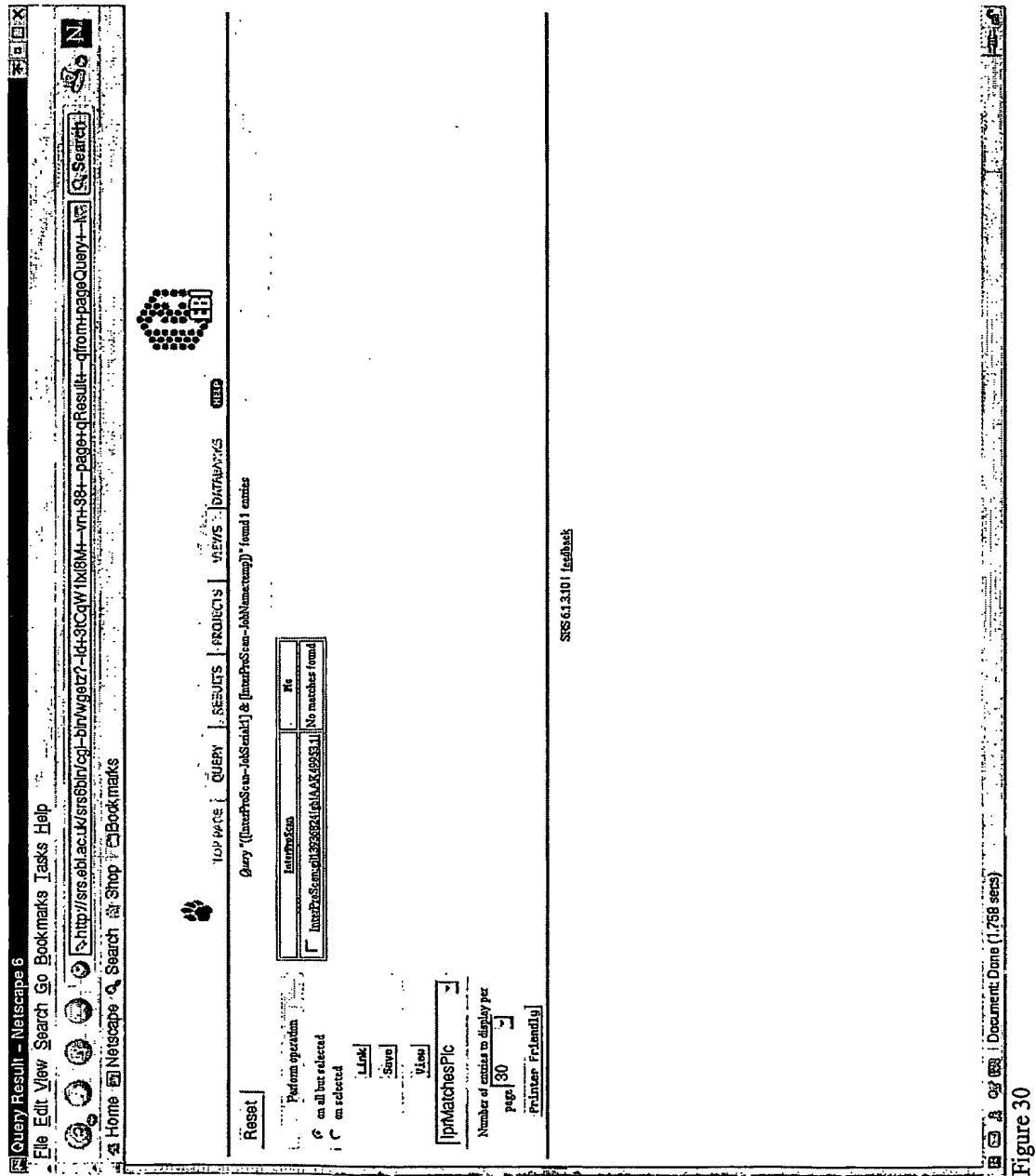
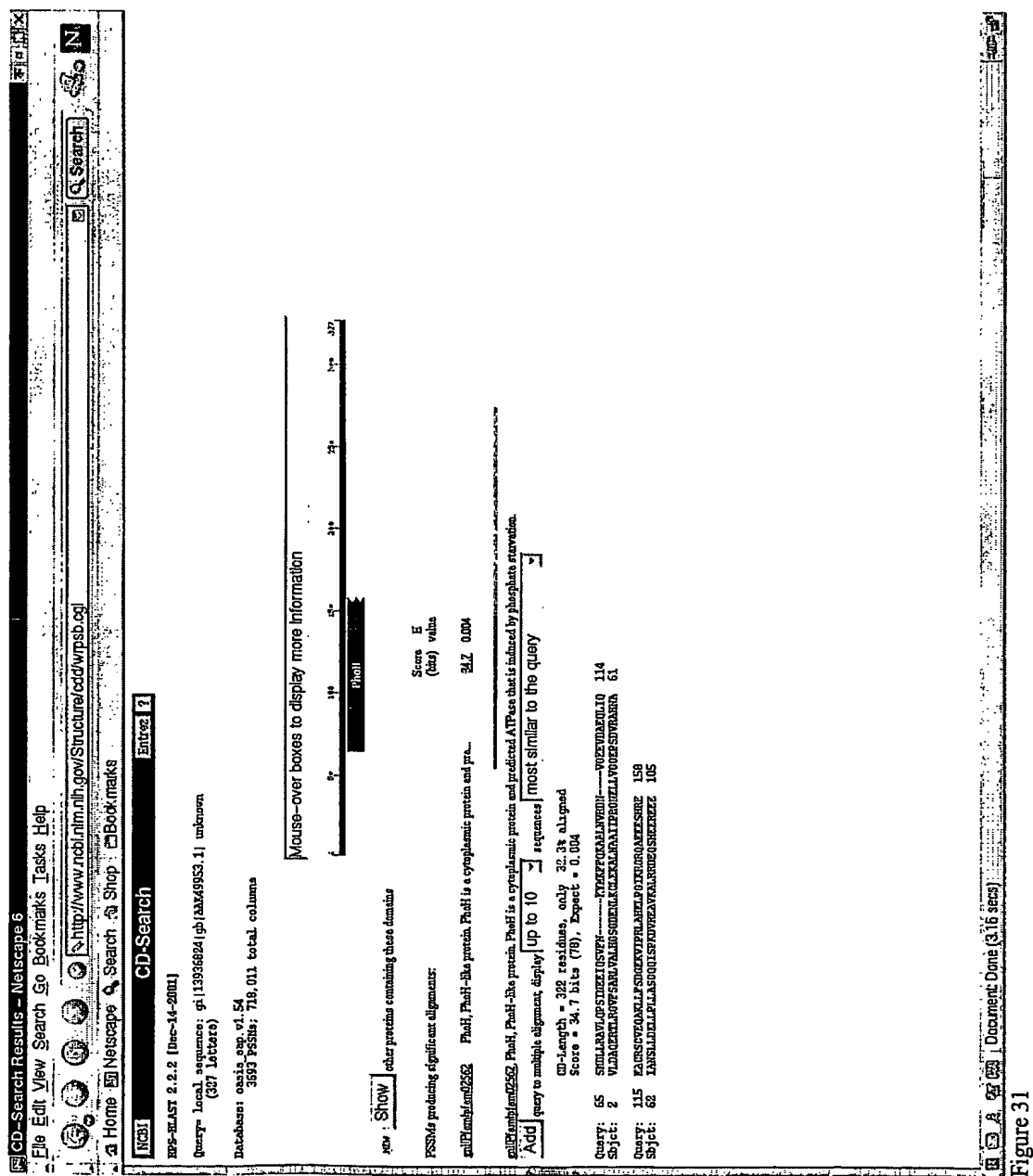


Figure 30



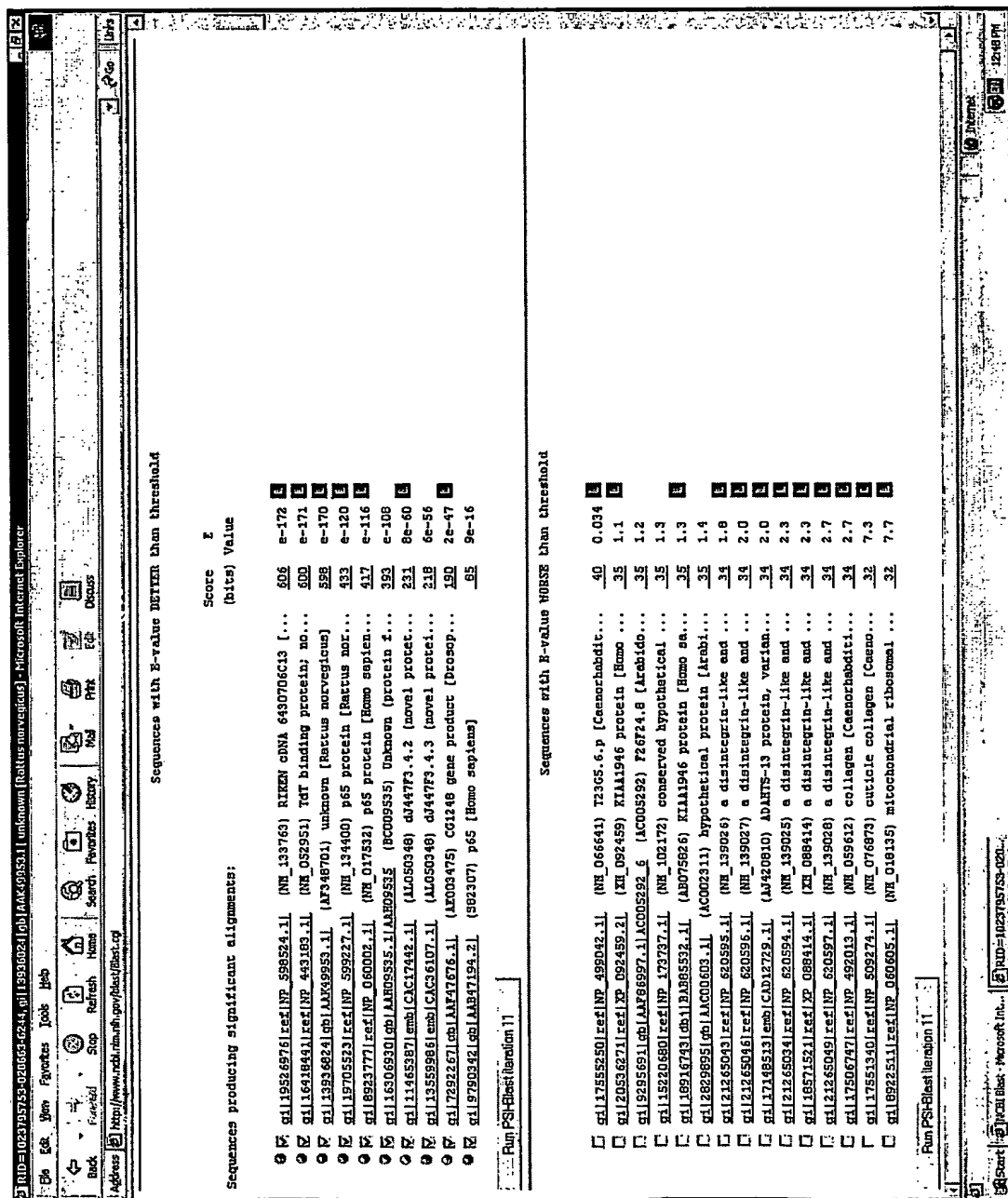


Figure 33

NCBI Sequence Viewer - Netscape 6

File Edit View Search Go Bookmarks Tasks Help

http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=protein&list_uids=19368248.cdp=GenPept Search

Home Ent Netscape Search Shop Bookmarks

S N C B I Protein

Search [Protein] [1] [er] [Lent]

Display default Save Text Add to Clipboard

Go Clear

Print

Clipboard

History

1:AAK4953 unknown [Rattus norvegicus] 327 aa Linear ROD 03-MAY-2001

LOCUS AAK4953 327 aa Linear ROD 03-MAY-2001
 DEFINITION unknown [Rattus norvegicus].
 ACCESSION AAK4953
 VERSION AAK4953.1 GI:1936824
 KEYWORDS locus AF348701 accession M248701.1
 SOURCE Norway rat.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (residues 1 to 327)
 Rat novel gene identified from uterus, highly expressed in rat
 prostate and CNS tissues
 JOURNAL Unpublished
 REFERENCE Long X., Bigby R.H. and Nephew K.P.
 Direct Sequencing of Rat Novel Gene Identified From Uterus,
 Prostate, and Brain Tissues. J Biol Chem 276(2001) 69079. Indiana University School of
 Medicine, 975 W Walnut Street, Indianapolis, IN 46202, USA
 METHOD conceptual translation.
 FEATURES
 source
 1..327
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 /db_xref="taxon:10116"
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 /feature_type="cds"
 1..327
 /product="unknown"
 1..327
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 /note="similar to Homo sapiens d14773.4.1 protein:
 Genbank Accession Number U51741"

ORIGIN
 1 agatctggc ggtcttgcg gcagacagg yrlgmnia lncqgrtg rsmctstf
 61 doaimdlr vlgpmias igwivnyk ffgcaaluv dnpsavdas qligaease
 121 kvvprlhf qsvprlhf ebgpkkrq acseahcep fpqrqvql ghvlandaa
 181 kvavrpfac eirrrgpcr qsrlnest fvlpvrnba lpgvftgr ytkhplfky
 241 admgddval acqhmarh qdgvlllas dirdlaad yrgvdikls elktvtlpsv
 301 nvcaktyas litrmehre aselpet
 //

RefSeq: October 24, 2001.

Showing 12 hits to the Basic Data
 NCBI BLAST tool

Figure 34

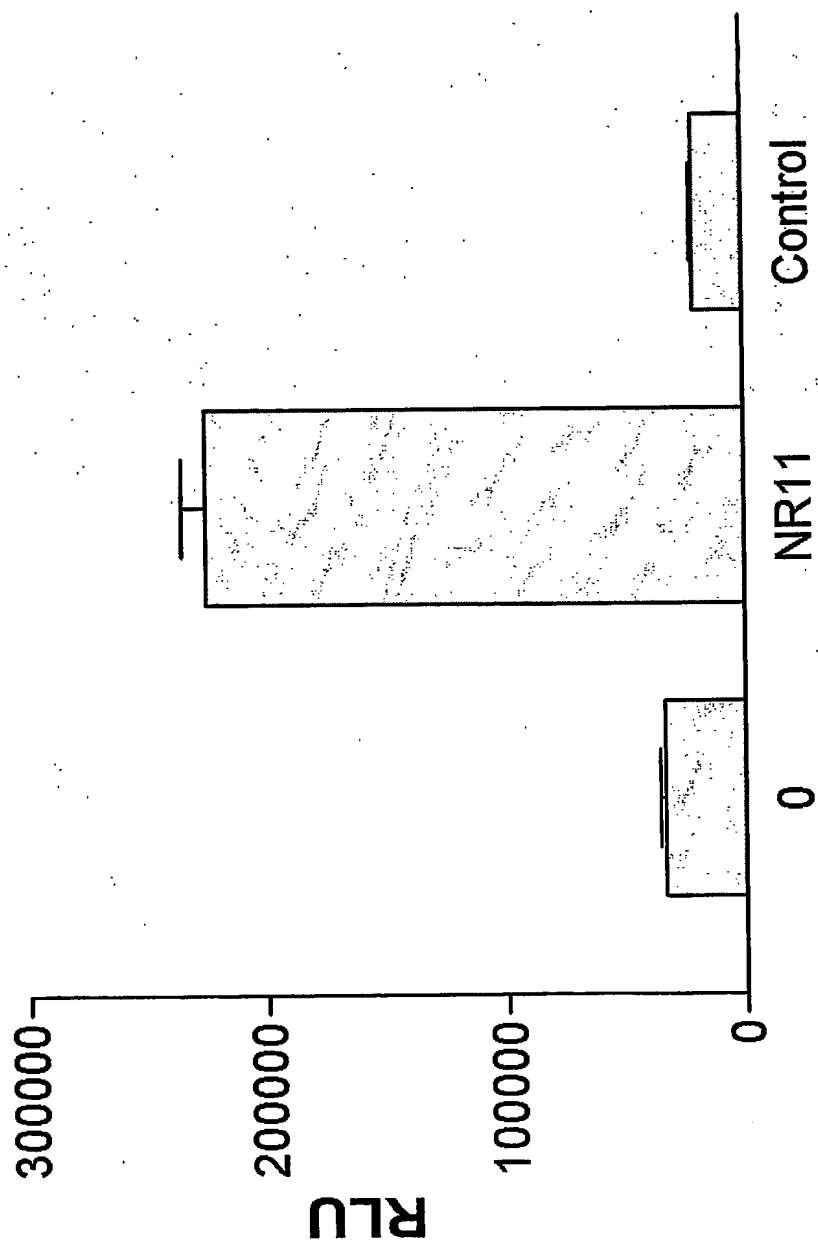


Figure 35

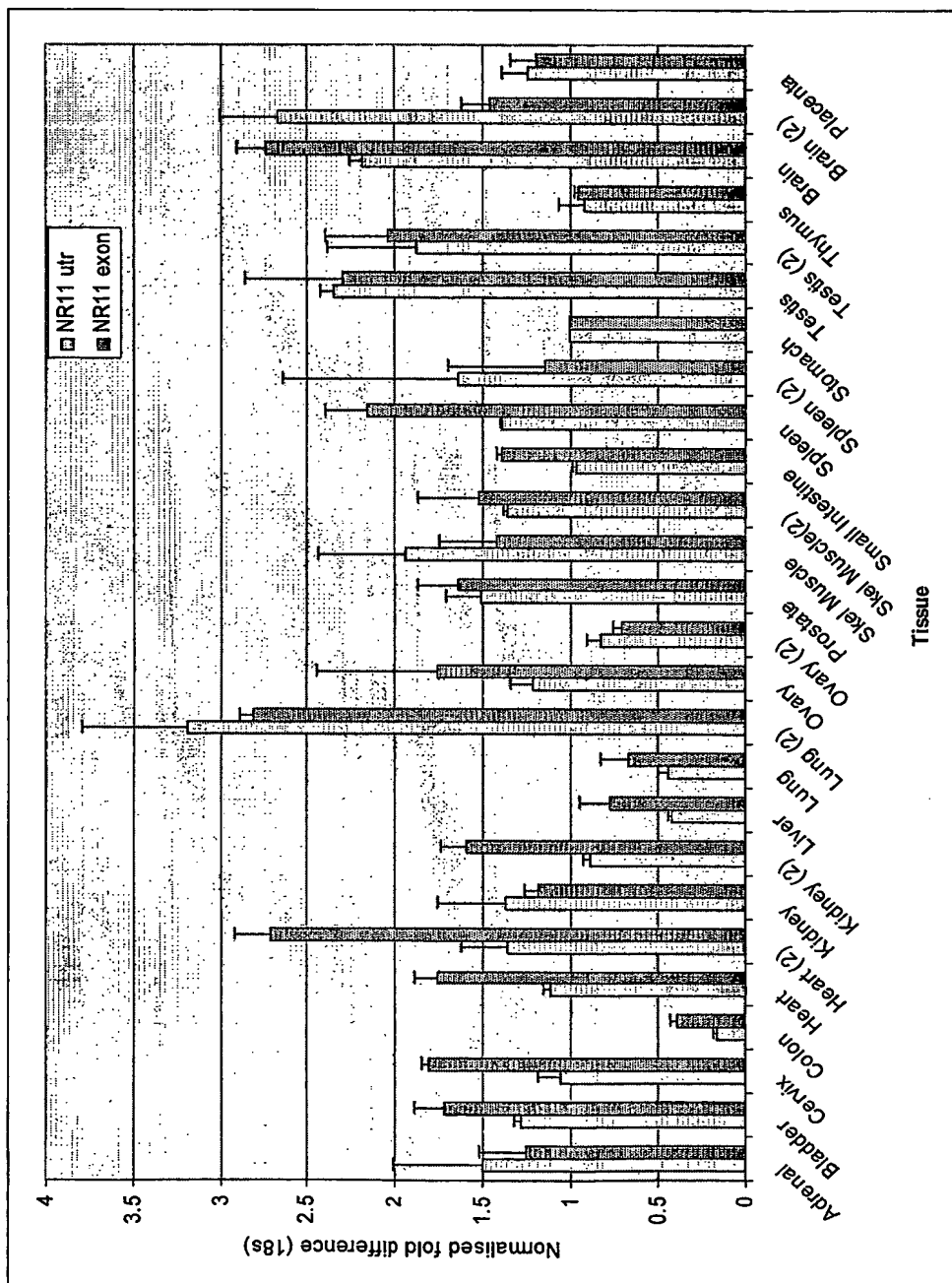


Figure 36

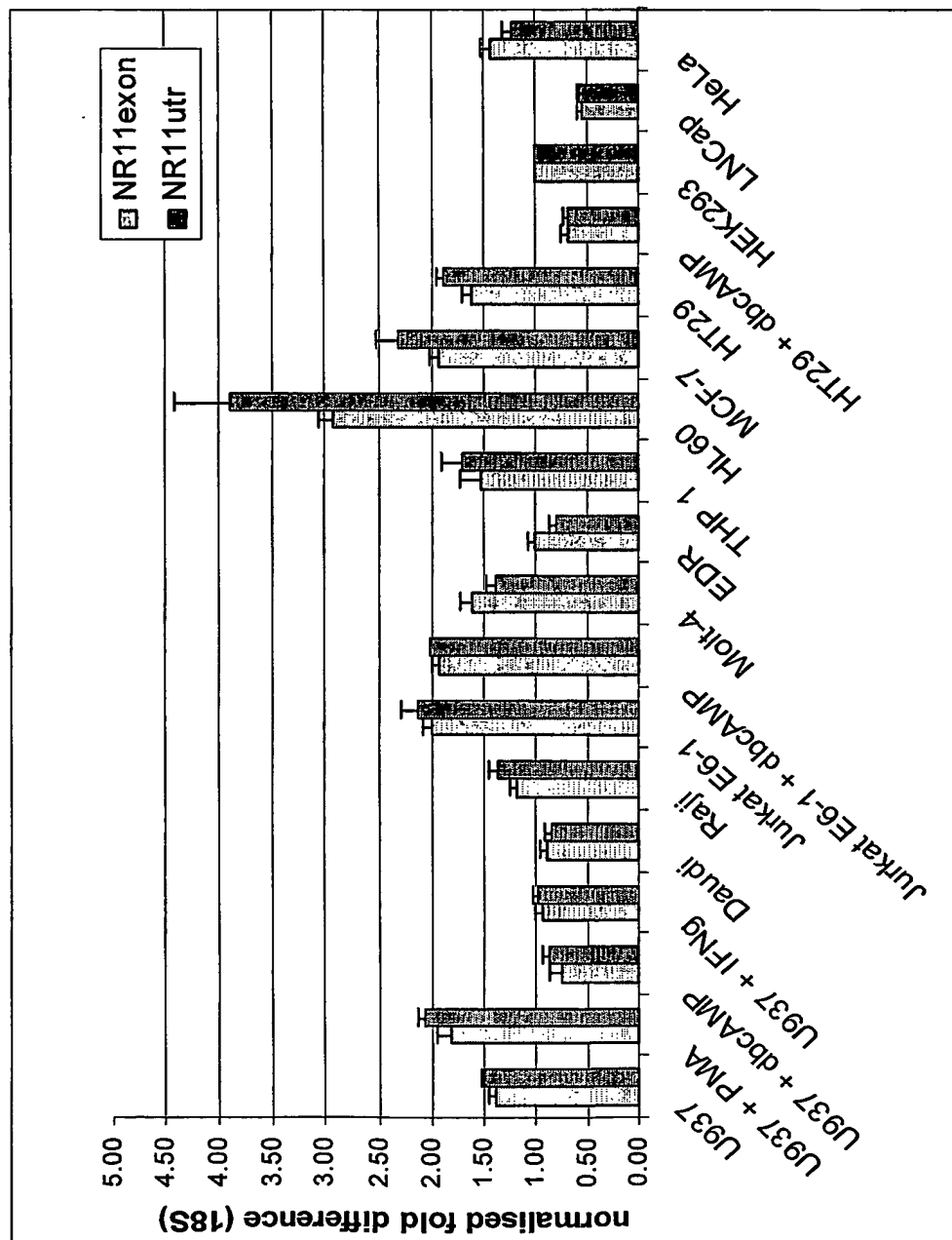


Figure 37

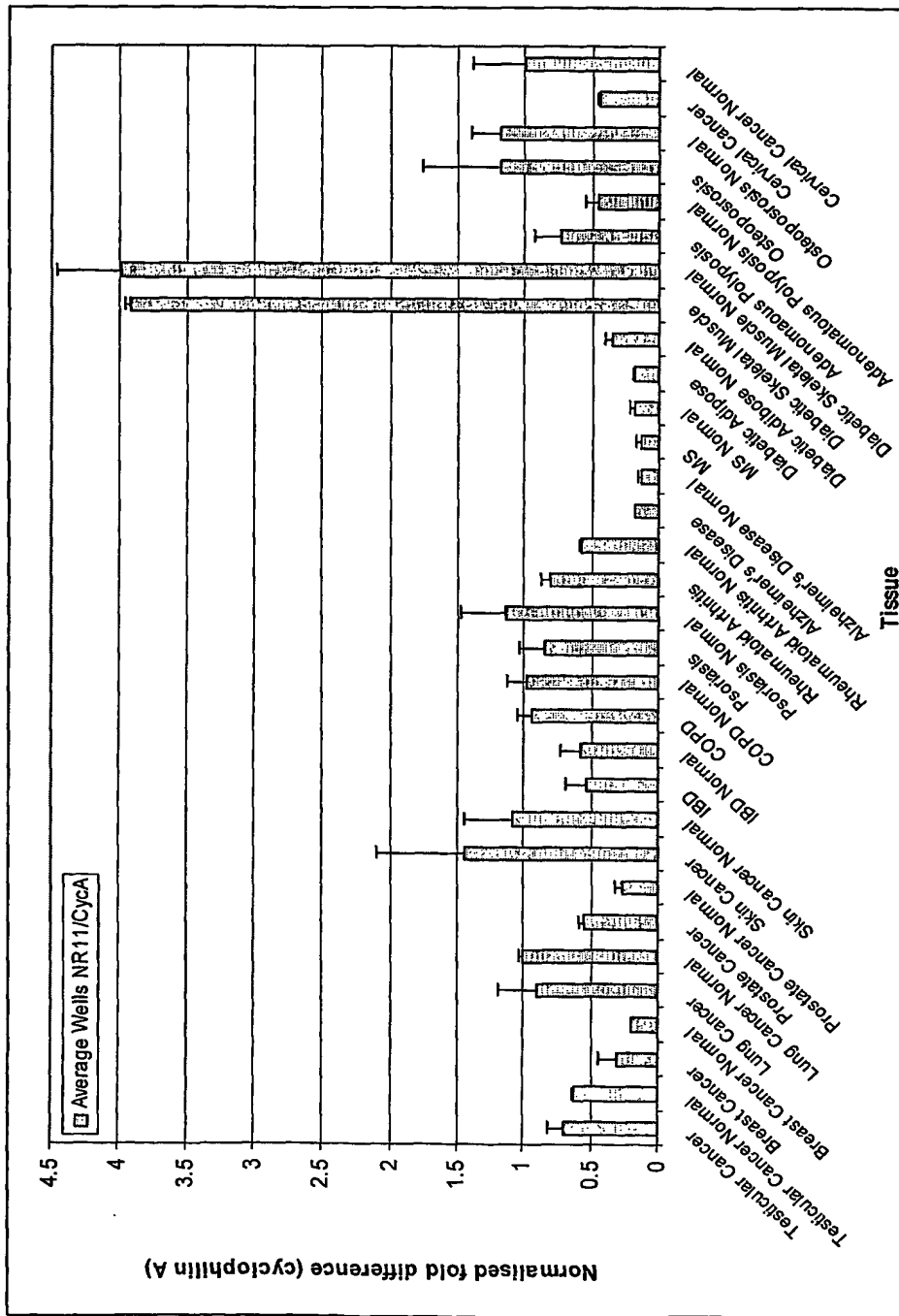


Figure 38

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